

#8

SEQUENCE LISTING

RECEIVED
MAY 03 2002
TECH CENTER 1600/2900

<110> Giuliano, Kenneth A.
Bright, Gary
Olson, Keith
Burroughs-Tencza, Sarah

<120> A System for Cell Based Screening

<130> 97-022-K2

<140> 09/713,572

<141> 2000-11-15

<150> 09/430,656

<151> 1999-10-29

<150> 09/398,965

<151> 1999-09-17

<150> 09/031,271

<151> 1998-02-27

<150> 08/810,983

<151> 1997-02-27

<150> 60/136,078

<151> 1999-05-26

<150> 60/106,308

<151> 1998-10-30

<160> 168

<170> PatentIn Ver. 2.0

<210> 1

<211> 1770

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (882)

<220>

<223> Description of Artificial Sequence:

GFP-DEVD-Annexin II construct

<400> 1

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc 720
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

gga ctc aga tct ggc gcc ggc gct gga gcc gga gct ggc gcc gga gcc 768
 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
 245 250 255

gac gag gtg gac ggc gcc ggc gcc gat gaa gta gat ggc gcc atg tct 816
 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
 260 265 270

act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gat cat tct 864
 Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser
 275 280 285

aca ccc cca agt gcc tat tgaatggtga gcaagggcga ggagctgttc 912
 Thr Pro Pro Ser Ala Tyr
 290

accgggggtgg tgcccatcct ggtcgagctg gacggcgacg taaacggcca caagttcagc 972
 gtgtccggcg agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc 1032
 accaccggca agctgcccgt gccctggccc accctcgtga ccaccctgac ctacggcgtg 1092
 cagtgttca gccgctaccc cgaccacatg aagcagcacg acttcttcaa gtccgccatg 1152
 cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc 1212
 cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc gcatcgagct gaagggcatc 1272
 gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac 1332
 aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc 1392
 cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa ccccccatc 1452
 ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc 1512
 aaagacccca acgagaagcg cgatcacatg gtctctgctgg agttcgtgac cgccgccggg 1572
 atcactctcg gcatggacga gctgtacaag tccggactca gatctggcgc cggcgctgga 1632
 gccggagctg gcgcccggagc cgacgaggtg gacggcgccg gcgccgatga agtagatggc 1692
 gccatgtcta ctgtccacga aatcctgtgc aagctcagct tggaggggtga tcattctaca 1752
 cccccaagtg cctattga 1770

<210> 2
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 GFP-DEVD-Annexin II construct

<400> 2
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
 245 250 255
 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
 260 265 270
 Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser
 275 280 285
 Thr Pro Pro Ser Ala Tyr
 290

<210> 3
 <211> 2439
 <212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (2436)

<220>

<223> Description of Artificial Sequence:

EYFP-DEVD-MAPKDM construct

<400> 3

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

180										185										190										
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624														
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu															
195					200					205																				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672														
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe															
210					215					220																				
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	aag	720														
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Lys															
225					230					235					240															
gga	gac	gaa	gtg	gac	gga	gcc	gac	ctc	agt	ctt	gtg	gat	gcg	ttg	aca	768														
Gly	Asp	Glu	Val	Asp	Gly	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr															
245					250					255																				
gaa	cca	cct	cca	gaa	att	gag	gga	gaa	ata	aag	cga	gac	ttc	atg	gct	816														
Glu	Pro	Pro	Pro	Glu	Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met	Ala															
260					265					270																				
gcg	ctg	gag	gca	gag	ccc	tat	gat	gac	atc	gtg	gga	gaa	act	gtg	gag	864														
Ala	Leu	Glu	Ala	Glu	Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val	Glu															
275					280					285																				
aaa	act	gag	ttt	att	cct	ctc	ctg	gat	ggg	gat	gag	aaa	acc	ggg	aac	912														
Lys	Thr	Glu	Phe	Ile	Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly	Asn															
290					295					300																				
tca	gag	tcc	aaa	aag	aaa	ccc	tgc	tta	gac	act	agc	cag	gtt	gaa	ggg	960														
Ser	Glu	Ser	Lys	Lys	Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu	Gly															
305					310					315					320															
atc	cca	tct	tct	aaa	cca	aca	ctc	cta	gcc	aat	ggg	gat	cat	gga	atg	1008														
Ile	Pro	Ser	Ser	Lys	Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly	Met															
325					330					335																				
gag	ggg	aat	aac	act	gca	ggg	tct	cca	act	gac	ttc	ctt	gaa	gag	aga	1056														
Glu	Gly	Asn	Asn	Thr	Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu	Arg															
340					345					350																				
gtg	gac	tat	ccg	gat	tat	cag	agc	agc	cag	aac	tgg	cca	gaa	gat	gca	1104														
Val	Asp	Tyr	Pro	Asp	Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp	Ala															
355					360					365																				
agc	ttt	tgt	ttc	cag	cct	cag	caa	gtg	tta	gat	act	gac	cag	gct	gag	1152														
Ser	Phe	Cys	Phe	Gln	Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala	Glu															
370					375					380																				
ccc	ttt	aac	gag	cac	cgt	gat	gat	ggg	ttg	gca	gat	ctg	ctc	ttt	gtc	1200														
Pro	Phe	Asn	Glu	His	Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe	Val															
385					390					395					400															
tcc	agt	gga	ccc	acg	aac	gct	tct	gca	ttt	aca	gag	cga	gac	aat	cct	1248														
Ser	Ser	Gly	Pro	Thr	Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn	Pro															
405					410					415																				

B1

tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg	1296
Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr	
420 425 430	
gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt	1344
Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys	
435 440 445	
tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca	1392
Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro	
450 455 460	
gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag	1440
Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln	
465 470 475 480	
ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg	1488
Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val	
485 490 495	
gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca	1536
Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala	
500 505 510	
gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg	1584
Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu	
515 520 525	
gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag	1632
Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln	
530 535 540	
gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc	1680
Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile	
545 550 555 560	
ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca	1728
Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro	
565 570 575	
cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa	1776
Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys	
580 585 590	
gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag	1824
Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu	
595 600 605	
gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg	1872
Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met	
610 615 620	
gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc	1920
Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg	
625 630 635 640	

tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag	1968
Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu	
645 650 655	
gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca	2016
Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr	
660 665 670	
ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg	2064
Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val	
675 680 685	
acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag	2112
Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu	
690 695 700	
aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct	2160
Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser	
705 710 715 720	
cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt	2208
Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu	
725 730 735	
cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa	2256
Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu	
740 745 750	
gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag	2304
Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu	
755 760 765	
gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att	2352
Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile	
770 775 780	
gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa	2400
Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu	
785 790 795 800	
aca aaa gta gca aca gtt cca att aaa gac aaa gga tga	2439
Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly	
805 810	

<210> 4
 <211> 812
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAPKDM construct

<400> 4
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys
 225 230 235 240
 Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu Val Asp Ala Leu Thr
 245 250 255
 Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala
 260 265 270
 Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu
 275 280 285
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300
 Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320

Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400
 Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620

Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 5
 <211> 2439
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2436)

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEAD-MAPKDM construct

<400> 5
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75						80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85						90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
		100						105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
	115					120						125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150				155						160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
			165					170						175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
		180					185						190				
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624	
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu		
		195				200						205					
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672	
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
	210					215					220						
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	ccc	720	
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Pro		
225					230			235							240		
aga	gac	gaa	gcc	gac	agc	gcc	gac	ctc	agt	ctt	gtg	gat	gcg	ttg	aca	768	
Arg	Asp	Glu	Ala	Asp	Ser	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr		

245										250										255										
gaa cca cct cca gaa att gag gga gaa ata aag cga gac ttc atg gct	816																													
Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala																														
260 265 270																														
gcg ctg gag gca gag ccc tat gat gac atc gtg gga gaa act gtg gag	864																													
Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu																														
275 280 285																														
aaa act gag ttt att cct ctc ctg gat ggt gat gag aaa acc ggg aac	912																													
Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn																														
290 295 300																														
tca gag tcc aaa aag aaa ccc tgc tta gac act agc cag gtt gaa ggt	960																													
Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly																														
305 310 315 320																														
atc cca tct tct aaa cca aca ctc cta gcc aat ggt gat cat gga atg	1008																													
Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met																														
325 330 335																														
gag ggg aat aac act gca ggg tct cca act gac ttc ctt gaa gag aga	1056																													
Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg																														
340 345 350																														
gtg gac tat ccg gat tat cag agc agc cag aac tgg cca gaa gat gca	1104																													
Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala																														
355 360 365																														
agc ttt tgt ttc cag cct cag caa gtg tta gat act gac cag gct gag	1152																													
Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu																														
370 375 380																														
ccc ttt aac gag cac cgt gat gat ggt ttg gca gat ctg ctc ttt gtc	1200																													
Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val																														
385 390 395 400																														
tcc agt gga ccc acg aac gct tct gca ttt aca gag cga gac aat cct	1248																													
Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro																														
405 410 415																														
tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg	1296																													
Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr																														
420 425 430																														
gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt	1344																													
Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys																														
435 440 445																														
tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca	1392																													
Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro																														
450 455 460																														
gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag	1440																													
Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln																														
465 470 475 480																														

ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg 1488
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495

gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca 1536
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510

gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg 1584
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525

gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag 1632
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540

gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc 1680
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560

ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca 1728
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575

cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa 1776
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590

gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag 1824
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605

gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg 1872
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620

gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc 1920
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640

tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag 1968
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655

gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca 2016
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670

ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg 2064
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685

acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag 2112
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700

aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct 2160
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt 2208
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa 2256
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag 2304
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att 2352
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa 2400
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 aca aaa gta gca aca gtt cca att aaa gac aaa gga tga 2439
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 6

<211> 812

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

EYFP-DEAD-MAPKDM construct

<400> 6

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Pro
 225 230 235 240
 Arg Asp Glu Ala Asp Ser Ala Asp Leu Ser Leu Val Asp Ala Leu Thr
 245 250 255
 Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala
 260 265 270
 Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu
 275 280 285
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300
 Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320
 Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400

Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700

Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 7
 <211> 864
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (861)

<220>
 <223> Description of Artificial Sequence: F25-MEK1
 construct

<400> 7
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac acc 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr
 225 230 235 240
 ggt atg ccc aag aag aag ccg acg ccc atc cag ctg aac ccg gcc ccc 768
 Gly Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro
 245 250 255
 gac ggc tct gca gtt aac ggg acc agc tct gcg gag acc aac ttg gag 816
 Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu
 260 265 270
 gcc ttg cag aag aag ctg gag gag cta gag ctt gat gag cag cag tga 864
 Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln
 275 280 285

<210> 8

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: F25-MEK1
construct

<400> 8

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr
225 230 235 240
Gly Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro
245 250 255
Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu
260 265 270
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln

275

280

285

<210> 9

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (873)

<220>

<223> Description of Artificial Sequence: F25-MEK2
construct

<400> 9

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac acc	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr	
225 230 235 240	
ggg atg ctg gcc cgg agg aag ccg gtg ctg ccg gcg ctc acc atc aac	768
Gly Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn	
245 250 255	
cct acc atc gcc gag ggc cca tcc cct acc agc gag ggc gcc tcc gag	816
Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu	
260 265 270	
gca aac ctg gtg gac ctg cag aag aag ctg gag gag ctg gaa ctt gac	864
Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp	
275 280 285	
gag cag cag taa	876
Glu Gln Gln	
290	

<210> 10
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: F25-MEK2
 construct

<400> 10
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50	55	60
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80		
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95		
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110		
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125		
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140		
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160		
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser 165 170 175		
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190		
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205		
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220		
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr 225 230 235 240		
Gly Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn 245 250 255		
Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu 260 265 270		
Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp 275 280 285		
Glu Gln Gln 290		

<210> 11
 <211> 889
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(888)

<220>

<223> Description of Artificial Sequence: Caspase
3-DEVD-substrate construct

<400> 11

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser	
225 230 235 240	
gga aga agg aaa cga caa aag cga tcg gct gtt aaa tct gaa gga aag	768
Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Val Lys Ser Glu Gly Lys	
245 250 255	
aga aag tgt gac gaa gtt gat gga att gat gaa gta gca agt act atg	816
Arg Lys Cys Asp Glu Val Asp Gly Ile Asp Glu Val Ala Ser Thr Met	
260 265 270	
tct act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat	864
Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His	
275 280 285	
tct aca ccc cca agt acc cgg atc c	889
Ser Thr Pro Pro Ser Thr Arg Ile	
290 295	

<210> 12
 <211> 296
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase
 3-DEVD-substrate construct

<400> 12

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	

bl

115					120					125					
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
130					135					140					
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					
Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
165					170					175					
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
180					185					190					
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
195					200					205					
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
210					215					220					
Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn	Ser
225					230					235					
Gly	Arg	Arg	Lys	Arg	Gln	Lys	Arg	Ser	Ala	Val	Lys	Ser	Glu	Gly	Lys
245					250					255					
Arg	Lys	Cys	Asp	Glu	Val	Asp	Gly	Ile	Asp	Glu	Val	Ala	Ser	Thr	Met
260					265					270					
Ser	Thr	Val	His	Glu	Ile	Leu	Cys	Lys	Leu	Ser	Leu	Glu	Gly	Val	His
275					280					285					
Ser	Thr	Pro	Pro	Ser	Thr	Arg	Ile								
290					295										

<210> 13
 <211> 846
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(846)

<220>
 <223> Description of Artificial Sequence: Caspase
 6-VEID-substrate construct

<400> 13
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

gga aga agg aaa cga caa aag cga tcg aca aga ctt gtt gaa att gac 768
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
 245 250 255

aac agt act atg agc aca gta cac gaa att tta tgt aaa tta agc tta 816
 Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 260 265 270

gaa gga gta cac agt aca cca cca agc gca 846
 Glu Gly Val His Ser Thr Pro Pro Ser Ala
 275 280

<210> 14
 <211> 282
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase
 6-VEID-substrate construct

<400> 14
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

B1

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
 245 250 255

Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 260 265 270

Glu Gly Val His Ser Thr Pro Pro Ser Ala
 275 280

<210> 15
 <211> 876
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(876)

<220>
 <223> Description of Artificial Sequence: Caspase 8-VETD
 construct

<400> 15
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125			384
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140			432
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160			480
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser 165 170 175			528
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190			576
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205			624
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220			672
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser 225 230 235 240			720
gga aga agc aaa cga caa aag cga tcg tat gaa aaa gga ata cca gtt Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val 245 250 255			768
gaa aca gac agc gaa gag caa gct tat agt act atg tct act gtc cac Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His 260 265 270			816
gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat tct aca ccc cca Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro 275 280 285			864
agt gcc gga tcc Ser Ala Gly Ser 290			876

<210> 16

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase 8-VETD
construct

<400> 16

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240

Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val
245 250 255

Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His
260 265 270

Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro
275 280 285

Ser Ala Gly Ser
290

<210> 17
<211> 906
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(906)

<220>
<223> Description of Artificial Sequence: Cas 3-multiple
DEVD construct

<400> 17
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn

145	150	155	160	
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc				528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	165	170	175	
ggt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc				576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt				624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195	200	205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt				672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc				720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser	225	230	235	240
gga aga agg aaa cga caa aag cga tcg gca ggt gac gaa gtt gat gca				768
Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala	245	250	255	
ggt gac gaa gtt gat gca ggt gac gaa gtt gat gca ggt gac gaa gtt				816
Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val	260	265	270	
gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc				864
Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu	275	280	285	
agc ttg gag ggt gtt cat tct aca ccc cca agt gcc gga tcc				906
Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser	290	295	300	

<210> 18

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cas 3-multiple
DEVD construct

<400> 18

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala
 245 250 255
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285
 Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 290 295 300

<210> 19
 <211> 906
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1)..(885)

<220>

<223> Description of Artificial Sequence: Caspase
8-multiple VETD construct

<400> 19

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	

195	200	205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc			720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser			
225	230	235	240
gga aga agg aaa cga caa aag cga tcg gca ggt gtt gaa aca gac gca			768
Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Val Glu Thr Asp Ala			
245	250	255	
ggg gtt gaa aca gac gca ggt gtt gaa aca gac gca ggt gtt gaa aca			816
Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr			
260	265	270	
gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc			864
Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu			
275	280	285	
agc ttg gag ggt gtt cat tct acacccccaa gtgccggatc c			906
Ser Leu Glu Gly Val His Ser			
290	295		

<210> 20
 <211> 295
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase
 8-multiple VETD construct

<400> 20
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Val Glu Thr Asp Ala
 245 250 255
 Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr
 260 265 270
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285
 Ser Leu Glu Gly Val His Ser
 290 295

<210> 21
 <211> 4833
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(4830)

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAP4-EBFP construct

<400> 21
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75						80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
			165					170						175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
			180				185						190				
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624	
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu		
		195					200					205					
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672	
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
	210					215					220						
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	aag	720	
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Lys		
	225				230				235						240		
gga	gac	gaa	gtg	gac	gga	atg	gcc	gac	ctc	agt	ctt	gtg	gat	gcg	ttg	768	
Gly	Asp	Glu	Val	Asp	Gly	Met	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu		

245										250										255										
aca	gaa	cca	cct	cca	gaa	att	gag	gga	gaa	ata	aag	cga	gac	ttc	atg	816														
Thr	Glu	Pro	Pro	Pro	Glu	Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met															
					260						265						270													
gct	gcg	ctg	gag	gca	gag	ccc	tat	gat	gac	atc	gtg	gga	gaa	act	gtg	864														
Ala	Ala	Leu	Glu	Ala	Glu	Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val															
					275						280						285													
gag	aaa	act	gag	ttt	att	cct	ctc	ctg	gat	ggg	gat	gag	aaa	acc	ggg	912														
Glu	Lys	Thr	Glu	Phe	Ile	Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly															
					290						295						300													
aac	tca	gag	tcc	aaa	aag	aaa	ccc	tgc	tta	gac	act	agc	cag	gtt	gaa	960														
Asn	Ser	Glu	Ser	Lys	Lys	Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu															
305						310						315						320												
ggg	atc	cca	tct	tct	aaa	cca	aca	ctc	cta	gcc	aat	ggg	gat	cat	gga	1008														
Gly	Ile	Pro	Ser	Ser	Lys	Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly															
					325						330						335													
atg	gag	ggg	aat	aac	act	gca	ggg	tct	cca	act	gac	ttc	ctt	gaa	gag	1056														
Met	Glu	Gly	Asn	Asn	Thr	Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu															
					340						345						350													
aga	gtg	gac	tat	ccg	gat	tat	cag	agc	agc	cag	aac	tgg	cca	gaa	gat	1104														
Arg	Val	Asp	Tyr	Pro	Asp	Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp															
					355						360						365													
gca	agc	ttt	tgt	ttc	cag	cct	cag	caa	gtg	tta	gat	act	gac	cag	gct	1152														
Ala	Ser	Phe	Cys	Phe	Gln	Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala															
					370						375						380													
gag	ccc	ttt	aac	gag	cac	cgt	gat	gat	ggg	ttg	gca	gat	ctg	ctc	ttt	1200														
Glu	Pro	Phe	Asn	Glu	His	Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe															
385						390						395						400												
gtc	tcc	agt	gga	ccc	acg	aac	gct	tct	gca	ttt	aca	gag	cga	gac	aat	1248														
Val	Ser	Ser	Gly	Pro	Thr	Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn															
					405						410						415													
cct	tca	gaa	gac	agt	tac	ggg	atg	ctt	ccc	tgt	gac	tca	ttt	gct	tcc	1296														
Pro	Ser	Glu	Asp	Ser	Tyr	Gly	Met	Leu	Pro	Cys	Asp	Ser	Phe	Ala	Ser															
					420						425						430													
acg	gct	gtt	gta	tct	cag	gag	tgg	tct	gtg	gga	gcc	cca	aac	tct	cca	1344														
Thr	Ala	Val	Val	Ser	Gln	Glu	Trp	Ser	Val	Gly	Ala	Pro	Asn	Ser	Pro															
					435						440						445													
tgt	tca	gag	tcc	tgt	gtc	tcc	cca	gag	gtt	act	ata	gaa	acc	cta	cag	1392														
Cys	Ser	Glu	Ser	Cys	Val	Ser	Pro	Glu	Val	Thr	Ile	Glu	Thr	Leu	Gln															
					450						455						460													
cca	gca	aca	gag	ctc	tcc	aag	gca	gca	gaa	gtg	gaa	tca	gtg	aaa	gag	1440														
Pro	Ala	Thr	Glu	Leu	Ser	Lys	Ala	Ala	Glu	Val	Glu	Ser	Val	Lys	Glu															
465						470						475						480												

bl

cag ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat	1488
Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp	
485 490 495	
gtg gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag	1536
Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu	
500 505 510	
gca gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata	1584
Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile	
515 520 525	
ttg gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc	1632
Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala	
530 535 540	
cag gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat	1680
Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn	
545 550 555 560	
atc ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca	1728
Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala	
565 570 575	
cca cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc	1776
Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro	
580 585 590	
aaa gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct	1824
Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro	
595 600 605	
gag gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc	1872
Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly	
610 615 620	
atg gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt	1920
Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val	
625 630 635 640	
cgc tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca	1968
Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr	
645 650 655	
gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca	2016
Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr	
660 665 670	
aca ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg	2064
Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu	
675 680 685	
gtg acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa	2112
Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys	
690 695 700	

gag aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg	2160
Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met	
705 710 715 720	
tct cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata	2208
Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile	
725 730 735	
ctt cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca	2256
Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser	
740 745 750	
gaa gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca	2304
Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr	
755 760 765	
gag gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg	2352
Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu	
770 775 780	
att gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg	2400
Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu	
785 790 795 800	
gaa aca aaa gta gca aca gtt cca att aaa gac aaa gga act gta cag	2448
Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly Thr Val Gln	
805 810 815	
act gaa gaa aaa cca cgt gaa gac tcc cag tta gca tct atg cag cac	2496
Thr Glu Glu Lys Pro Arg Glu Asp Ser Gln Leu Ala Ser Met Gln His	
820 825 830	
aag gga cag tca aca gta cct cct tgc acg gct tca cca gaa cca gtc	2544
Lys Gly Gln Ser Thr Val Pro Pro Cys Thr Ala Ser Pro Glu Pro Val	
835 840 845	
aaa gct gca gaa caa atg tct acc tta cca ata gat gca cct tct cca	2592
Lys Ala Ala Glu Gln Met Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro	
850 855 860	
tta gag aac tta gag cag aag gaa acg cct ggc agc cag cct tct gag	2640
Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu	
865 870 875 880	
cct tgc tca gga gta tcc cgg caa gaa gaa gca aag gct gct gta ggt	2688
Pro Cys Ser Gly Val Ser Arg Gln Glu Glu Ala Lys Ala Ala Val Gly	
885 890 895	
gtg act gga aat gac atc act acc ccg cca aac aag gag cca cca cca	2736
Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro	
900 905 910	
agc cca gaa aag aaa gca aag cct ttg gcc acc act caa cct gca aag	2784
Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys	
915 920 925	
act tca aca tcg aaa gcc aaa aca cag ccc act tct ctc cct aag caa	2832

Thr	Ser	Thr	Ser	Lys	Ala	Lys	Thr	Gln	Pro	Thr	Ser	Leu	Pro	Lys	Gln		
930						935					940						
cca	gct	ccc	acc	acc	tct	ggg	ggg	ttg	aat	aaa	aaa	ccc	atg	agc	ctc	2880	
Pro	Ala	Pro	Thr	Thr	Ser	Gly	Gly	Leu	Asn	Lys	Lys	Pro	Met	Ser	Leu		
945					950				955						960		
gcc	tca	ggc	tca	gtg	cca	gct	gcc	cca	cac	aaa	cgc	cct	gct	gct	gcc	2928	
Ala	Ser	Gly	Ser	Val	Pro	Ala	Ala	Pro	His	Lys	Arg	Pro	Ala	Ala	Ala		
				965				970						975			
act	gct	act	gcc	agg	cct	tcc	acc	cta	cct	gcc	aga	gac	gtg	aag	cca	2976	
Thr	Ala	Thr	Ala	Arg	Pro	Ser	Thr	Leu	Pro	Ala	Arg	Asp	Val	Lys	Pro		
			980					985					990				
aag	cca	att	aca	gaa	gct	aag	gtt	gcc	gaa	aag	cgg	acc	tct	cca	tcc	3024	
Lys	Pro	Ile	Thr	Glu	Ala	Lys	Val	Ala	Glu	Lys	Arg	Thr	Ser	Pro	Ser		
	995					1000					1005						
aag	cct	tca	tct	gcc	cca	gcc	ctc	aaa	cct	gga	cct	aaa	acc	acc	cca	3072	
Lys	Pro	Ser	Ser	Ala	Pro	Ala	Leu	Lys	Pro	Gly	Pro	Lys	Thr	Thr	Pro		
	1010					1015				1020							
acc	gtt	tca	aaa	gcc	aca	tct	ccc	tca	act	ctt	gtt	tcc	act	gga	cca	3120	
Thr	Val	Ser	Lys	Ala	Thr	Ser	Pro	Ser	Thr	Leu	Val	Ser	Thr	Gly	Pro		
1025					1030				1035					1040			
agt	agt	aga	agt	cca	gct	aca	act	ctg	cct	aag	agg	cca	acc	agc	atc	3168	
Ser	Ser	Arg	Ser	Pro	Ala	Thr	Thr	Leu	Pro	Lys	Arg	Pro	Thr	Ser	Ile		
				1045				1050						1055			
aag	act	gag	ggg	aaa	cct	gct	gat	gtc	aaa	agg	atg	act	gct	aag	tct	3216	
Lys	Thr	Glu	Gly	Lys	Pro	Ala	Asp	Val	Lys	Arg	Met	Thr	Ala	Lys	Ser		
		1060						1065					1070				
gcc	tca	gct	gac	ttg	agt	cgc	tca	aag	acc	acc	tct	gcc	agt	tct	gtg	3264	
Ala	Ser	Ala	Asp	Leu	Ser	Arg	Ser	Lys	Thr	Thr	Ser	Ala	Ser	Ser	Val		
		1075					1080					1085					
aag	aga	aac	acc	act	ccc	act	ggg	gca	gca	ccc	cca	gca	ggg	atg	act	3312	
Lys	Arg	Asn	Thr	Thr	Pro	Thr	Gly	Ala	Ala	Pro	Pro	Ala	Gly	Met	Thr		
	1090					1095				1100							
tcc	act	cga	gtc	aag	ccc	atg	tct	gca	cct	agc	cgc	tct	tct	ggg	gct	3360	
Ser	Thr	Arg	Val	Lys	Pro	Met	Ser	Ala	Pro	Ser	Arg	Ser	Ser	Gly	Ala		
1105					1110				1115					1120			
ctt	tct	gtg	gac	aag	aag	ccc	act	tcc	act	aag	cct	agc	tcc	tct	gct	3408	
Leu	Ser	Val	Asp	Lys	Lys	Pro	Thr	Ser	Thr	Lys	Pro	Ser	Ser	Ser	Ala		
			1125					1130						1135			
ccc	agg	gtg	agc	cgc	ctg	gcc	aca	act	gtt	tct	gcc	cct	gac	ctg	aag	3456	
Pro	Arg	Val	Ser	Arg	Leu	Ala	Thr	Thr	Val	Ser	Ala	Pro	Asp	Leu	Lys		
			1140					1145					1150				
agt	gtt	cgc	tcc	aag	gtc	ggc	tct	aca	gaa	aac	atc	aaa	cac	cag	cct	3504	
Ser	Val	Arg	Ser	Lys	Val	Gly	Ser	Thr	Glu	Asn	Ile	Lys	His	Gln	Pro		

1155	1160	1165	
gga gga ggc cgg gcc aaa gta gag aaa aaa aca gag gca gct acc aca Gly Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr 1170 1175 1180			3552
gct ggg aag cct gaa cct aat gca gtc act aaa gca gcc ggc tcc att Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile 1185 1190 1195 1200			3600
gcg agt gca cag aaa ccg cct gct ggg aaa gtc cag ata gta tcc aaa Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys 1205 1210 1215			3648
aaa gtg agc tac agt cat att caa tcc aag tgt gtt tcc aag gac aat Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn 1220 1225 1230			3696
att aag cat gtc cct gga tgt ggc aat gtt cag att cag aac aag aaa Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys 1235 1240 1245			3744
gtg gac ata tcc aag gtc tcc tcc aag tgt ggg tcc aaa gct aat atc Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile 1250 1255 1260			3792
aag cac aag cct ggt gga gga gat gtc aag att gaa agt cag aag ttg Lys His Lys Pro Gly Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu 1265 1270 1275 1280			3840
aac ttc aag gag aag gcc caa gcc aaa gtg gga tcc ctt gat aac gtt Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val 1285 1290 1295			3888
ggc cac ttt cct gca gga ggt gcc gtg aag act gag ggc ggt ggc agt Gly His Phe Pro Ala Gly Gly Ala Val Lys Thr Glu Gly Gly Gly Ser 1300 1305 1310			3936
gag gcc ctt ccg tgt cca ggc ccc ccc gct ggg gag gag cca gtc atc Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile 1315 1320 1325			3984
cct gag gct gcg cct gac cgt ggc gcc cct act tca gcc agt ggc ctc Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu 1330 1335 1340			4032
agt ggc cac acc acc ctg tca ggg ggt ggt gac caa agg gag ccc cag Ser Gly His Thr Thr Leu Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln 1345 1350 1355 1360			4080
acc ttg gac agc cag atc cag gag aca agc atc atg gtg agc aag ggc Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly 1365 1370 1375			4128
gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly 1380 1385 1390			4176

gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat 4224
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
1395 1400 1405

gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag 4272
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
1410 1415 1420

ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg 4320
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val
1425 1430 1435 1440

cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc 4368
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
1445 1450 1455

aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc 4416
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
1460 1465 1470

aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc 4464
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
1475 1480 1485

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 4512
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1490 1495 1500

gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac 4560
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His
1505 1510 1515 1520

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac 4608
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
1525 1530 1535

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 4656
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
1540 1545 1550

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 4704
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
1555 1560 1565

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 4752
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
1570 1575 1580

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 4800
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
1585 1590 1595 1600

atc act ctc ggc atg gac gag ctg tac aag tag 4833
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
1605 1610

<210> 22
 <211> 1610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAP4-EBFP construct

<400> 22
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys
 225 230 235 240
 Gly Asp Glu Val Asp Gly Met Ala Asp Leu Ser Leu Val Asp Ala Leu

245										250					255				
Thr	Glu	Pro	Pro	Pro	Glu	Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met				
			260					265					270						
Ala	Ala	Leu	Glu	Ala	Glu	Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val				
		275					280					285							
Glu	Lys	Thr	Glu	Phe	Ile	Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly				
	290					295				300									
Asn	Ser	Glu	Ser	Lys	Lys	Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu				
305					310					315					320				
Gly	Ile	Pro	Ser	Ser	Lys	Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly				
				325				330						335					
Met	Glu	Gly	Asn	Asn	Thr	Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu				
			340					345					350						
Arg	Val	Asp	Tyr	Pro	Asp	Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp				
		355					360					365							
Ala	Ser	Phe	Cys	Phe	Gln	Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala				
	370					375					380								
Glu	Pro	Phe	Asn	Glu	His	Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe				
385					390					395					400				
Val	Ser	Ser	Gly	Pro	Thr	Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn				
				405					410					415					
Pro	Ser	Glu	Asp	Ser	Tyr	Gly	Met	Leu	Pro	Cys	Asp	Ser	Phe	Ala	Ser				
			420					425					430						
Thr	Ala	Val	Val	Ser	Gln	Glu	Trp	Ser	Val	Gly	Ala	Pro	Asn	Ser	Pro				
		435					440					445							
Cys	Ser	Glu	Ser	Cys	Val	Ser	Pro	Glu	Val	Thr	Ile	Glu	Thr	Leu	Gln				
	450					455					460								
Pro	Ala	Thr	Glu	Leu	Ser	Lys	Ala	Ala	Glu	Val	Glu	Ser	Val	Lys	Glu				
465					470				475						480				
Gln	Leu	Pro	Ala	Lys	Ala	Leu	Glu	Thr	Met	Ala	Glu	Gln	Thr	Thr	Asp				
				485					490					495					
Val	Val	His	Ser	Pro	Ser	Thr	Asp	Thr	Thr	Pro	Gly	Pro	Asp	Thr	Glu				
			500					505					510						
Ala	Ala	Leu	Ala	Lys	Asp	Ile	Glu	Glu	Ile	Thr	Lys	Pro	Asp	Val	Ile				
		515					520					525							
Leu	Ala	Asn	Val	Thr	Gln	Pro	Ser	Thr	Glu	Ser	Asp	Met	Phe	Leu	Ala				
	530					535					540								
Gln	Asp	Met	Glu	Leu	Leu	Thr	Gly	Thr	Glu	Ala	Ala	His	Ala	Asn	Asn				

545		550		555		560
Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala						
		565		570		575
Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro						
		580		585		590
Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro						
		595		600		605
Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly						
		610		615		620
Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val						
		625		630		635
Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr						
		645		650		655
Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr						
		660		665		670
Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu						
		675		680		685
Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys						
		690		695		700
Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met						
		705		710		715
Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile						
		725		730		735
Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser						
		740		745		750
Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr						
		755		760		765
Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu						
		770		775		780
Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu						
		785		790		795
Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly Thr Val Gln						
		805		810		815
Thr Glu Glu Lys Pro Arg Glu Asp Ser Gln Leu Ala Ser Met Gln His						
		820		825		830
Lys Gly Gln Ser Thr Val Pro Pro Cys Thr Ala Ser Pro Glu Pro Val						
		835		840		845
Lys Ala Ala Glu Gln Met Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro						

850 855 860
 Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu
 865 870 875 880
 Pro Cys Ser Gly Val Ser Arg Gln Glu Glu Ala Lys Ala Ala Val Gly
 885 890 895
 Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro
 900 905 910
 Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys
 915 920 925
 Thr Ser Thr Ser Lys Ala Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln
 930 935 940
 Pro Ala Pro Thr Thr Ser Gly Gly Leu Asn Lys Lys Pro Met Ser Leu
 945 950 955 960
 Ala Ser Gly Ser Val Pro Ala Ala Pro His Lys Arg Pro Ala Ala Ala
 965 970 975
 Thr Ala Thr Ala Arg Pro Ser Thr Leu Pro Ala Arg Asp Val Lys Pro
 980 985 990
 Lys Pro Ile Thr Glu Ala Lys Val Ala Glu Lys Arg Thr Ser Pro Ser
 995 1000 1005
 Lys Pro Ser Ser Ala Pro Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro
 1010 1015 1020
 Thr Val Ser Lys Ala Thr Ser Pro Ser Thr Leu Val Ser Thr Gly Pro
 1025 1030 1035 1040
 Ser Ser Arg Ser Pro Ala Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile
 1045 1050 1055
 Lys Thr Glu Gly Lys Pro Ala Asp Val Lys Arg Met Thr Ala Lys Ser
 1060 1065 1070
 Ala Ser Ala Asp Leu Ser Arg Ser Lys Thr Thr Ser Ala Ser Ser Val
 1075 1080 1085
 Lys Arg Asn Thr Thr Pro Thr Gly Ala Ala Pro Pro Ala Gly Met Thr
 1090 1095 1100
 Ser Thr Arg Val Lys Pro Met Ser Ala Pro Ser Arg Ser Ser Gly Ala
 1105 1110 1115 1120
 Leu Ser Val Asp Lys Lys Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala
 1125 1130 1135
 Pro Arg Val Ser Arg Leu Ala Thr Thr Val Ser Ala Pro Asp Leu Lys
 1140 1145 1150
 Ser Val Arg Ser Lys Val Gly Ser Thr Glu Asn Ile Lys His Gln Pro

1155	1160	1165
Gly Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr 1170 1175 1180		
Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile 1185 1190 1195 1200		
Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys 1205 1210 1215		
Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn 1220 1225 1230		
Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys 1235 1240 1245		
Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile 1250 1255 1260		
Lys His Lys Pro Gly Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu 1265 1270 1275 1280		
Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val 1285 1290 1295		
Gly His Phe Pro Ala Gly Gly Ala Val Lys Thr Glu Gly Gly Gly Ser 1300 1305 1310		
Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile 1315 1320 1325		
Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu 1330 1335 1340		
Ser Gly His Thr Thr Leu Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln 1345 1350 1355 1360		
Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly 1365 1370 1375		
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly 1380 1385 1390		
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp 1395 1400 1405		
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys 1410 1415 1420		
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val 1425 1430 1435 1440		
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe 1445 1450 1455		
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe		

1460	1465	1470
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly		
1475	1480	1485
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu		
1490	1495	1500
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His		
1505	1510	1515
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn		
1525	1530	1535
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp		
1540	1545	1550
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro		
1555	1560	1565
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn		
1570	1575	1580
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly		
1585	1590	1595
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		
1605	1610	

<210> 23
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence:
 GFP-nucleolus-Caspase 8-annexin II construct

<400> 23

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50						55					60						
ctg	tgc	tat	ggg	gtt	caa	tgc	ttt	tca	aga	tac	ccg	gat	cat	atg	aaa	240	
Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	80	
65					70				75								
cgg	cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggg	tat	gta	cag	gaa	288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	95	
				85					90								
agg	acc	atc	ttc	ttc	aaa	gat	gac	ggc	aac	tac	aag	aca	cgt	gct	gaa	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	110	
			100					105									
gtc	aag	ttt	gaa	ggg	gat	acc	ctt	gtt	aat	aga	atc	gag	tta	aaa	ggg	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	125	
		115					120										
att	gac	ttc	aag	gaa	gat	ggc	aac	att	ctg	gga	cac	aaa	ttg	gaa	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	140	
	130					135											
aac	tat	aac	tca	cac	aat	gta	tac	atc	atg	gca	gac	aaa	caa	aag	aat	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	160	
145					150					155							
gga	atc	aaa	gtg	aac	ttc	aag	acc	cgc	cac	aac	att	gaa	gat	gga	agc	528	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	175	
				165					170								
gtt	caa	cta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat	ggc	576	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	190	
			180					185									
cct	gtc	ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	aca	caa	tct	gcc	ctt	624	
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	205	
		195					200										
tcg	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	ctt	ctt	gag	ttt	672	
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	220	
	210					215											
gta	aca	gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	ctg	tac	aac	tcc	720	
Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn	Ser	240	
225					230				235								
gga	aga	aaa	cgt	ata	cgt	act	tac	ctc	aag	tcc	tgc	agg	cgg	atg	aaa	768	
Gly	Arg	Lys	Arg	Ile	Arg	Thr	Tyr	Leu	Lys	Ser	Cys	Arg	Arg	Met	Lys	255	
				245					250								
aga	agt	ggg	ttt	gag	atg	tct	cga	cct	att	cct	tcc	cac	ctt	act	cga	816	
Arg	Ser	Gly	Phe	Glu	Met	Ser	Arg	Pro	Ile	Pro	Ser	His	Leu	Thr	Arg	270	
			260					265									
tcg	gca	ggg	gtt	gaa	aca	gac	gca	ggg	gtt	gaa	aca	gac	gca	ggg	gtt	864	
Ser	Ala	Gly	Val	Glu	Thr	Asp	Ala	Gly	Val	Glu	Thr	Asp	Ala	Gly	Val		

bl

275	280	285	
gaa aca gac gca ggt gtt	gaa aca gac gca ggt	agt act atg tct act	912
Glu Thr Asp Ala Gly Val	Glu Thr Asp Ala Gly	Ser Thr Met Ser Thr	
290	295	300	
gtc cac gaa atc ctg tgc	aag ctc agc ttg gag	ggg gtt cat tct aca	960
Val His Glu Ile Leu Cys	Lys Leu Ser Leu Glu	Gly Val His Ser Thr	
305	310	315	320
ccc cca agt gcc gga tcc			978
Pro Pro Ser Ala Gly Ser			
325			

<210> 24

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

GFP-nucleolus-Caspase 8-annexin II construct

<400> 24

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240

Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys
245 250 255

Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg
260 265 270

Ser Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val
275 280 285

Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Ser Thr Met Ser Thr
290 295 300

Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr
305 310 315 320

Pro Pro Ser Ala Gly Ser
325

<210> 25
<211> 948
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (948)

<220>
<223> Description of Artificial Sequence:
GFP-nucleolus-Caspase 3-annexin II construct

<400> 25
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser	
225 230 235 240	
gga aga aaa cgt ata cgt act tac ctc aag tcc tgc agg cgg atg aaa	768
Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys	
245 250 255	
aga agt ggt ttt gag atg tct cga cct att cct tcc cac ctt act cga	816
Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg	
260 265 270	

tcg tat gaa aaa gga ata cca gtt gaa aca gac agc gaa gag caa gct 864
 Ser Tyr Glu Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Ala
 275 280 285

tat agt act atg tct act gtc cac gaa atc ctg tgc aag ctc agc ttg 912
 Tyr Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 290 295 300

gag ggt gtt cat tct aca ccc cca agt gcc gga tcc 948
 Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 305 310 315

<210> 26

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

GFP-nucleolus-Caspase 3-annexin II construct

<400> 26

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

180										185					190						
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu						
		195					200					205									
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe						
	210					215				220											
Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Asn	Ser						
225					230				235						240						
Gly	Arg	Lys	Arg	Ile	Arg	Thr	Tyr	Leu	Lys	Ser	Cys	Arg	Arg	Met	Lys						
				245					250					255							
Arg	Ser	Gly	Phe	Glu	Met	Ser	Arg	Pro	Ile	Pro	Ser	His	Leu	Thr	Arg						
		260						265					270								
Ser	Tyr	Glu	Lys	Gly	Ile	Pro	Val	Glu	Thr	Asp	Ser	Glu	Glu	Gln	Ala						
	275					280					285										
Tyr	Ser	Thr	Met	Ser	Thr	Val	His	Glu	Ile	Leu	Cys	Lys	Leu	Ser	Leu						
	290					295					300										
Glu	Gly	Val	His	Ser	Thr	Pro	Pro	Ser	Ala	Gly	Ser										
305					310					315											

<210> 27
 <211> 2106
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1050)

<220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-cellubrevin construct

<400> 27
 atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act 48
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15
 gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac 96
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30
 aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa 144
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 35 40 45
 ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg 192
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60

cca aca cta gtc act act ctg tgc tat ggt gtt caa tgc ttt tca aga	240
Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg	
65 70 75 80	
tac ccg gat cat atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc	288
Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro	
85 90 95	
gaa ggt tat gta cag gaa agg acc atc ttc ttc aaa gat gac ggc aac	336
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn	
100 105 110	
tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat	384
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn	
115 120 125	
aga atc gag tta aaa ggt att gac ttc aag gaa gat ggc aac att ctg	432
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu	
130 135 140	
gga cac aaa ttg gaa tac aac tat aac tca cac aat gta tac atc atg	480
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met	
145 150 155 160	
gca gac aaa caa aag aat gga atc aaa gtg aac ttc aag acc cgc cac	528
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His	
165 170 175	
aac att gaa gat gga agc gtt caa cta gca gac cat tat caa caa aat	576
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn	
180 185 190	
act cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg	624
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu	
195 200 205	
tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag aga gac cac	672
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His	
210 215 220	
atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg	720
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met	
225 230 235 240	
gat gaa ctg tac aac acc ggt atg tct aca ggt gtg cct tcg ggg tca	768
Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Val Pro Ser Gly Ser	
245 250 255	
agt gct gcc act ggc agt aat cga aga ctc cag cag aca caa aat caa	816
Ser Ala Ala Thr Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln	
260 265 270	
gta gat gag gtg gtt gac atc atg aga gtc aat gtg gat aag gtg tta	864
Val Asp Glu Val Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu	
275 280 285	
gaa aga gac cag aag ctc tcg gag cta gat gac cgc gca gat gca ctg	912

Glu	Arg	Asp	Gln	Lys	Leu	Ser	Glu	Leu	Asp	Asp	Arg	Ala	Asp	Ala	Leu	
290						295					300					

cag	gca	ggt	gcc	tcg	cag	ttt	gaa	aca	agt	gct	gcc	aag	ttg	aag	aga	960
Gln	Ala	Gly	Ala	Ser	Gln	Phe	Glu	Thr	Ser	Ala	Ala	Lys	Leu	Lys	Arg	
305					310					315					320	

aag	tat	tgg	tgg	aag	aac	tgc	aag	atg	tgg	gcg	ata	ggg	atc	agt	gtc	1008
Lys	Tyr	Trp	Trp	Lys	Asn	Cys	Lys	Met	Trp	Ala	Ile	Gly	Ile	Ser	Val	
				325					330					335		

ctg	gtg	atc	att	gtc	atc	atc	atc	atc	gtg	tgg	tgt	gtc	tct			1050
Leu	Val	Ile	Ile	Val	Ile	Ile	Ile	Ile	Val	Trp	Cys	Val	Ser			
				340					345				350			

taaatgagaa gaaaacgaca aaaggctagc aaaggagaag aactcttcac tggagttgtc 1110

ccaattcttg ttgaattaga tggatgatgtt aacggccaca agttctctgt cagtggagag 1170

ggtgaagggtg atgcaacata cggaaaactt accctgaagt tcatctgcac tactggcaaa 1230

ctgcctgttc catggccaac actagtcact actctgtgct atgggtgttca atgcttttca 1290

agatacccggt atcatatgaa acggcatgac tttttcaaga gtgccatgcc cgaagggttat 1350

gtacaggaaa ggaccatctt cttcaaagat gacggcaact acaagacacg tgctgaagtc 1410

aagtttgaag gtgataccct tgttaataga atcgagttaa aaggatttga cttcaaggaa 1470

gatggcaaca ttctgggaca caaattggaa tacaactata actcacacaa tgtatacatc 1530

atggcagaca aacaaaagaa tggaatcaaa gtgaacttca agaccgcga caacattgaa 1590

gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgatggccct 1650

gtccttttac cagacaacca ttacctgtcc acacaatctg ccctttcgaa agatcccaac 1710

gaaaagagag accacatggt ctttcttgag tttgtaacag ctgctgggat tacacatggc 1770

atggatgaac tgtacaacac cggatgtgtc acaggtgtgc cttcggggtc aagtgtgcc 1830

actggcagta atcgaagact ccagcagaca caaatcaag tagatgaggt ggttgacatc 1890

atgagagtca atgtggataa ggtgttagaa agagaccaga agctctcgga gctagatgac 1950

cgcgagatg cactgcaggc aggtgcctcg cagtttgaaa caagtgtgc caagttgaag 2010

agaaagtatt ggtggaagaa ctgcaagatg tgggcgatag ggatcagtg cctggtgatc 2070

attgtcatca tcatcatcgt gtggtgtgtc tcttaa 2106

<210> 28
 <211> 350
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
NLS-Fred25-cellubrevin construct

<400> 28

Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
1 5 10 15

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
20 25 30

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
35 40 45

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
50 55 60

Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
65 70 75 80

Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
85 90 95

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
100 105 110

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
115 120 125

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
130 135 140

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
145 150 155 160

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
165 170 175

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
180 185 190

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
195 200 205

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
210 215 220

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
225 230 235 240

Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Val Pro Ser Gly Ser
245 250 255

Ser Ala Ala Thr Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln
260 265 270

Val Asp Glu Val Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu

275	280	285
Glu Arg Asp Gln Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu		
290	295	300
Gln Ala Gly Ala Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg		
305	310	315
Lys Tyr Trp Trp Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Ser Val		
325	330	335
Leu Val Ile Ile Val Ile Ile Ile Ile Val Trp Cys Val Ser		
340	345	350

<210> 29
 <211> 2088
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1041)

<220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-synaptobrevin construct

<400> 29

atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act	48
Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr	
1 5 10 15	
gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac	96
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His	
20 25 30	
aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa	144
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys	
35 40 45	
ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg	192
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp	
50 55 60	
cca aca cta gtc act act ctg tgc tat ggt gtt caa tgc ttt tca aga	240
Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg	
65 70 75 80	
tac ccg gat cat atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc	288
Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro	
85 90 95	
gaa ggt tat gta cag gaa agg acc atc ttc ttc aaa gat gac ggc aac	336
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn	
100 105 110	

tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat 384
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 115 120 125

aga atc gag tta aaa ggt att gac ttc aag gaa gat ggc aac att ctg 432
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 130 135 140

gga cac aaa ttg gaa tac aac tat aac tca cac aat gta tac atc atg 480
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 145 150 155 160

gca gac aaa caa aag aat gga atc aaa gtg aac ttc aag acc cgc cac 528
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 165 170 175

aac att gaa gat gga agc gtt caa cta gca gac cat tat caa caa aat 576
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 180 185 190

act cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg 624
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 195 200 205

tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag aga gac cac 672
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 210 215 220

atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg 720
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 225 230 235 240

gat gaa ctg tac aac acc ggt atg tct aca ggt cca act gct gcc act 768
 Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Pro Thr Ala Ala Thr
 245 250 255

ggc agt aat cga aga ctt cag cag aca caa aat caa gta gat gag gtg 816
 Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln Val Asp Glu Val
 260 265 270

gtg gac ata atg cga gtt aac gtg gac aag gtt ctg gaa aga gac cag 864
 Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu Glu Arg Asp Gln
 275 280 285

aag ctc tct gag tta gac gac cgt gca gac gca ctg cag gca ggc gct 912
 Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu Gln Ala Gly Ala
 290 295 300

tct caa ttt gaa acg agc gca gcc aag ttg aag agg aaa tat tgg tgg 960
 Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg Lys Tyr Trp Trp
 305 310 315 320

aag aat tgc aag atg tgg gca atc ggg att act gtt ctg gtt atc ttc 1008
 Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe
 325 330 335

atc atc atc atc atc gtg tgg gtt gtc tct tca tgaatgagaa gaaaacgaca 1061

Ile Ile Ile Ile Ile Val Trp Val Val Ser Ser
340 345

aaaggctagc aaaggagaag aactcttcac tggagttgtc ccaattcttg ttgaattaga 1121
tggtgatggt aacggccaca agttctctgt cagtggagag ggtgaagggtg atgcaacata 1181
cggaaaactt accctgaagt tcatctgcac tactggcaaa ctgcctgttc catggccaac 1241
actagtcact actctgtgct atgggtgttca atgcttttca agatacccg atcatatgaa 1301
acggcatgac tttttcaaga gtgccatgcc cgaaggttat gtacaggaaa ggaccatctt 1361
cttcaaagat gacggcaact acaagacacg tgctgaagtc aagtttgaag gtgataccct 1421
tggttaataga atcgagttaa aaggatttga cttcaaggaa gatggcaaca ttctgggaca 1481
caaattggaa tacaactata actcacacaa tgtatacatc atggcagaca aacaaaagaa 1541
tggaatcaaa gtgaacttca agaccgcga caacattgaa gatggaagcg ttcaactagc 1601
agaccattat caacaaaata ctccaattgg cgatggccct gtccttttac cagacaacca 1661
ttacctgtcc acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt 1721
ccttcttgag tttgtaacag ctgctgggat tacacatggc atggatgaac tgtacaacac 1781
cggtatgtct acaggtccaa ctgctgccac tggcagtaat cgaagacttc agcagacaca 1841
aaatcaagta gatgaggtgg tggacataat gcgagttaac gtggacaagg ttctggaaag 1901
agaccagaag ctctctgagt tagacgaccg tgcagacgca ctgcaggcag gcgcttctca 1961
atttgaaacg agcgagcca agttgaagag gaaatattgg tggaagaatt gcaagatgtg 2021
ggcaatcggg attactgttc tggttatctt catcatcatc atcatcgtgt gggttgtctc 2081
ttcatga 2088

<210> 30
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
NLS-Fred25-synaptobrevin construct

b1
<400> 30
Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
1 5 10 15
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
20 25 30
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys

35					40					45					
Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp
50						55					60				
Pro	Thr	Leu	Val	Thr	Thr	Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg
65					70					75					80
Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro
				85					90					95	
Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn
			100					105					110		
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn
		115					120					125			
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu
	130					135					140				
Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met
145					150					155					160
Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Thr	Arg	His
				165					170					175	
Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn
		180						185					190		
Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu
		195					200					205			
Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His
		210					215				220				
Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met
225					230					235					240
Asp	Glu	Leu	Tyr	Asn	Thr	Gly	Met	Ser	Thr	Gly	Pro	Thr	Ala	Ala	Thr
				245					250					255	
Gly	Ser	Asn	Arg	Arg	Leu	Gln	Gln	Thr	Gln	Asn	Gln	Val	Asp	Glu	Val
			260					265					270		
Val	Asp	Ile	Met	Arg	Val	Asn	Val	Asp	Lys	Val	Leu	Glu	Arg	Asp	Gln
		275					280					285			
Lys	Leu	Ser	Glu	Leu	Asp	Asp	Arg	Ala	Asp	Ala	Leu	Gln	Ala	Gly	Ala
	290					295					300				
Ser	Gln	Phe	Glu	Thr	Ser	Ala	Ala	Lys	Leu	Lys	Arg	Lys	Tyr	Trp	Trp
305					310					315					320
Lys	Asn	Cys	Lys	Met	Trp	Ala	Ile	Gly	Ile	Thr	Val	Leu	Val	Ile	Phe
				325					330					335	
Ile	Ile	Ile	Ile	Ile	Val	Trp	Val	Val	Ser	Ser					

340

345

<210> 31
 <211> 3171
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(3168)

<220>
 <223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 31
 atg agg ccc aga aga aag gtg agc aag ggc gag gag ctg ttc acc ggg 48
 Met Arg Pro Arg Arg Lys Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
 1 5 10 15
 gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag 96
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 20 25 30
 ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg 144
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 35 40 45
 acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc 192
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 50 55 60
 acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac 240
 Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr
 65 70 75 80
 ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa 288
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 85 90 95
 ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac 336
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 100 105 110
 aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc 384
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 115 120 125
 atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg 432
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 130 135 140
 cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc 480
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 145 150 155 160

gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac	528
Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
165 170 175	
atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc	576
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
180 185 190	
ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc	624
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
195 200 205	
tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg	672
Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met	
210 215 220	
gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac	720
Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	
225 230 235 240	
gag ctg tac aag aag gga gac gaa gtg gac gga gcc gac ctc agt ctt	768
Glu Leu Tyr Lys Lys Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu	
245 250 255	
gtg gat gcg ttg aca gaa cca cct cca gaa att gag gga gaa ata aag	816
Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys	
260 265 270	
cga gac ttc atg gct gcg ctg gag gca gag ccc tat gat gac atc gtg	864
Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val	
275 280 285	
gga gaa act gtg gag aaa act gag ttt att cct ctc ctg gat ggt gat	912
Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp	
290 295 300	
gag aaa acc ggg aac tca gag tcc aaa aag aaa ccc tgc tta gac act	960
Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr	
305 310 315 320	
agc cag gtt gaa ggt atc cca tct tct aaa cca aca ctc cta gcc aat	1008
Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn	
325 330 335	
ggt gat cat gga atg gag ggg aat aac act gca ggg tct cca act gac	1056
Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp	
340 345 350	
ttc ctt gaa gag aga gtg gac tat ccg gat tat cag agc agc cag aac	1104
Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn	
355 360 365	
tggt cca gaa gat gca agc ttt tgt ttc cag cct cag caa gtg tta gat	1152
Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp	
370 375 380	
act gac cag gct gag ccc ttt aac gag cac cgt gat gat ggt ttg gca	1200

Thr	Asp	Gln	Ala	Glu	Pro	Phe	Asn	Glu	His	Arg	Asp	Asp	Gly	Leu	Ala		
385					390					395					400		
gat	ctg	ctc	ttt	gtc	tcc	agt	gga	ccc	acg	aac	gct	tct	gca	ttt	aca	1248	
Asp	Leu	Leu	Phe	Val	Ser	Ser	Gly	Pro	Thr	Asn	Ala	Ser	Ala	Phe	Thr		
				405					410					415			
gag	cga	gac	aat	cct	tca	gaa	gac	agt	tac	ggg	atg	ctt	ccc	tgt	gac	1296	
Glu	Arg	Asp	Asn	Pro	Ser	Glu	Asp	Ser	Tyr	Gly	Met	Leu	Pro	Cys	Asp		
			420					425					430				
tca	ttt	gct	tcc	acg	gct	gtt	gta	tct	cag	gag	tgg	tct	gtg	gga	gcc	1344	
Ser	Phe	Ala	Ser	Thr	Ala	Val	Val	Ser	Gln	Glu	Trp	Ser	Val	Gly	Ala		
			435				440						445				
cca	aac	tct	cca	tgt	tca	gag	tcc	tgt	gtc	tcc	cca	gag	gtt	act	ata	1392	
Pro	Asn	Ser	Pro	Cys	Ser	Glu	Ser	Cys	Val	Ser	Pro	Glu	Val	Thr	Ile		
			450			455					460						
gaa	acc	cta	cag	cca	gca	aca	gag	ctc	tcc	aag	gca	gca	gaa	gtg	gaa	1440	
Glu	Thr	Leu	Gln	Pro	Ala	Thr	Glu	Leu	Ser	Lys	Ala	Ala	Glu	Val	Glu		
					470				475						480		
tca	gtg	aaa	gag	cag	ctg	cca	gct	aaa	gca	ttg	gaa	acg	atg	gca	gag	1488	
Ser	Val	Lys	Glu	Gln	Leu	Pro	Ala	Lys	Ala	Leu	Glu	Thr	Met	Ala	Glu		
				485				490						495			
cag	acc	act	gat	gtg	gtg	cac	tct	cca	tcc	aca	gac	aca	aca	cca	ggc	1536	
Gln	Thr	Thr	Asp	Val	Val	His	Ser	Pro	Ser	Thr	Asp	Thr	Thr	Pro	Gly		
			500					505					510				
cca	gac	aca	gag	gca	gca	ctg	gct	aaa	gac	ata	gaa	gag	atc	acc	aag	1584	
Pro	Asp	Thr	Glu	Ala	Ala	Leu	Ala	Lys	Asp	Ile	Glu	Glu	Ile	Thr	Lys		
			515				520					525					
cca	gat	gtg	ata	ttg	gca	aat	gtc	acg	cag	cca	tct	act	gaa	tcg	gat	1632	
Pro	Asp	Val	Ile	Leu	Ala	Asn	Val	Thr	Gln	Pro	Ser	Thr	Glu	Ser	Asp		
			530			535					540						
atg	ttc	ctg	gcc	cag	gac	atg	gaa	cta	ctc	aca	gga	aca	gag	gca	gcc	1680	
Met	Phe	Leu	Ala	Gln	Asp	Met	Glu	Leu	Leu	Thr	Gly	Thr	Glu	Ala	Ala		
					550					555					560		
cac	gct	aac	aat	atc	ata	ttg	cct	aca	gaa	cca	gac	gaa	tct	tca	acc	1728	
His	Ala	Asn	Asn	Ile	Ile	Leu	Pro	Thr	Glu	Pro	Asp	Glu	Ser	Ser	Thr		
				565				570						575			
aag	gat	gta	gca	cca	cct	atg	gaa	gaa	gaa	att	gtc	cca	ggc	aat	gat	1776	
Lys	Asp	Val	Ala	Pro	Pro	Met	Glu	Glu	Glu	Ile	Val	Pro	Gly	Asn	Asp		
				580				585					590				
acg	aca	tcc	ccc	aaa	gaa	aca	gag	aca	aca	ctt	cca	ata	aaa	atg	gac	1824	
Thr	Thr	Ser	Pro	Lys	Glu	Thr	Glu	Thr	Thr	Leu	Pro	Ile	Lys	Met	Asp		
			595				600					605					
ttg	gca	cca	cct	gag	gat	gtg	tta	ctt	acc	aaa	gaa	aca	gaa	cta	gcc	1872	
Leu	Ala	Pro	Pro	Glu	Asp	Val	Leu	Leu	Thr	Lys	Glu	Thr	Glu	Leu	Ala		

610	615	620	
cca gcc aag ggc atg gtt tca ctc tca gaa ata gaa gag gct ctg gca Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala 625 630 635 640			1920
aag aat gat gtt cgc tct gca gaa ata cct gtg gct cag gag aca gtg Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val 645 650 655			1968
gtc tca gaa aca gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser 660 665 670			2016
gat ccc ata aca aca ttg aca aag gat gtg aca ctc ccc tta gaa gca Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala 675 680 685			2064
gag aga ccg ttg gtg acg gac atg act cca tct ctg gaa aca gaa atg Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met 690 695 700			2112
acc cta ggc aaa gag aca gct cca ccc aca gaa aca aat ttg ggc atg Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met 705 710 715 720			2160
gcc aaa gac atg tct cca ctc cca gaa tca gaa gtg act ctg ggc aag Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys 725 730 735			2208
gac gtg gtt ata ctt cca gaa aca aag gtg gct gag ttt aac aat gtg Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val 740 745 750			2256
act cca ctt tca gaa gaa gag gta acc tca gtc aag gac atg tct ccg Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro 755 760 765			2304
tct gca gaa aca gag gct ccc ctg gct aag aat gct gat ctg cac tca Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser 770 775 780			2352
gga aca gag ctg att gtg gac aac agc atg gct cca gcc tcc gat ctt Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu 785 790 795 800			2400
gca ctg ccc ttg gaa aca aaa gta gca aca gtt cca att aaa gac aaa Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys 805 810 815			2448
gga atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 820 825 830			2496
ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 835 840 845			2544

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 2592
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 850 855 860

 atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 2640
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 865 870 875 880

 acc ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 2688
 Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 885 890 895

 aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 2736
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 900 905 910

 gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 2784
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 915 920 925

 gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 2832
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 930 935 940

 ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 2880
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 945 950 955 960

 tac aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 2928
 Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 965 970 975

 aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 2976
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 980 985 990

 agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 3024
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 995 1000 1005

 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 3072
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1010 1015 1020

 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 3120
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040

 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 3168
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

 tag 3171

<210> 32

<211> 1056
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 32

Met	Arg	Pro	Arg	Arg	Lys	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	1	5	10	15
Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	20	25	30	
Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	35	40	45	
Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	50	55	60	
Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	65	70	75	80
Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	85	90	95	
Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	100	105	110	
Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	115	120	125	
Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	130	135	140	
His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	145	150	155	160
Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	165	170	175	
Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	180	185	190	
Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	195	200	205	
Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	210	215	220	
Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	225	230	235	240
Glu	Leu	Tyr	Lys	Lys	Gly	Asp	Glu	Val	Asp	Gly	Ala	Asp	Leu	Ser	Leu	245	250	255	

Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys
 260 265 270
 Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val
 275 280 285
 Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp
 290 295 300
 Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr
 305 310 315 320
 Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn
 325 330 335
 Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp
 340 345 350
 Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn
 355 360 365
 Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp
 370 375 380
 Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala
 385 390 395 400
 Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr
 405 410 415
 Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp
 420 425 430
 Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala
 435 440 445
 Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile
 450 455 460
 Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu
 465 470 475 480
 Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu
 485 490 495
 Gln Thr Thr Asp Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly
 500 505 510
 Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys
 515 520 525
 Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp
 530 535 540
 Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala
 545 550 555 560

His	Ala	Asn	Asn	Ile	Ile	Leu	Pro	Thr	Glu	Pro	Asp	Glu	Ser	Ser	Thr	
				565					570					575		
Lys	Asp	Val	Ala	Pro	Pro	Met	Glu	Glu	Glu	Ile	Val	Pro	Gly	Asn	Asp	
			580				585					590				
Thr	Thr	Ser	Pro	Lys	Glu	Thr	Glu	Thr	Thr	Leu	Pro	Ile	Lys	Met	Asp	
		595					600					605				
Leu	Ala	Pro	Pro	Glu	Asp	Val	Leu	Leu	Thr	Lys	Glu	Thr	Glu	Leu	Ala	
	610					615					620					
Pro	Ala	Lys	Gly	Met	Val	Ser	Leu	Ser	Glu	Ile	Glu	Glu	Ala	Leu	Ala	
625					630					635					640	
Lys	Asn	Asp	Val	Arg	Ser	Ala	Glu	Ile	Pro	Val	Ala	Gln	Glu	Thr	Val	
				645					650					655		
Val	Ser	Glu	Thr	Glu	Val	Val	Leu	Ala	Thr	Glu	Val	Val	Leu	Pro	Ser	
			660					665					670			
Asp	Pro	Ile	Thr	Thr	Leu	Thr	Lys	Asp	Val	Thr	Leu	Pro	Leu	Glu	Ala	
		675					680					685				
Glu	Arg	Pro	Leu	Val	Thr	Asp	Met	Thr	Pro	Ser	Leu	Glu	Thr	Glu	Met	
	690					695					700					
Thr	Leu	Gly	Lys	Glu	Thr	Ala	Pro	Pro	Thr	Glu	Thr	Asn	Leu	Gly	Met	
705					710					715					720	
Ala	Lys	Asp	Met	Ser	Pro	Leu	Pro	Glu	Ser	Glu	Val	Thr	Leu	Gly	Lys	
				725					730					735		
Asp	Val	Val	Ile	Leu	Pro	Glu	Thr	Lys	Val	Ala	Glu	Phe	Asn	Asn	Val	
			740					745					750			
Thr	Pro	Leu	Ser	Glu	Glu	Glu	Val	Thr	Ser	Val	Lys	Asp	Met	Ser	Pro	
		755					760					765				
Ser	Ala	Glu	Thr	Glu	Ala	Pro	Leu	Ala	Lys	Asn	Ala	Asp	Leu	His	Ser	
	770					775					780					
Gly	Thr	Glu	Leu	Ile	Val	Asp	Asn	Ser	Met	Ala	Pro	Ala	Ser	Asp	Leu	
785					790					795					800	
Ala	Leu	Pro	Leu	Glu	Thr	Lys	Val	Ala	Thr	Val	Pro	Ile	Lys	Asp	Lys	
				805					810					815		
Gly	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	
			820					825					830			
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	
		835					840					845				
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	
	850					855					860					

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 865 870 875 880
 Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 885 890 895
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 900 905 910
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 915 920 925
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 930 935 940
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 945 950 955 960
 Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 965 970 975
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 980 985 990
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 995 1000 1005
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1010 1015 1020
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

<210> 33
 <211> 1623
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1623)

<220>
 <223> Description of Artificial Sequence:
 YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 33
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20					25					30						
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
35				40				45								
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50			55				60									
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65		70				75				80						
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
85				90				95								
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
100			105				110									
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
115			120				125									
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
130			135				140									
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145		150				155				160						
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
165				170				175								
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
180			185				190									
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	
195			200				205									
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
210		215				220										
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
225		230				235				240						
gga	aga	agg	aaa	cga	caa	aag	cga	tcg	gca	ggg	gac	gaa	gtt	gat	gca	768
Gly	Arg	Arg	Lys	Arg	Gln	Lys	Arg	Ser	Ala	Gly	Asp	Glu	Val	Asp	Ala	
245				250				255								

ggt gac gaa gtt gat gca ggt gac gaa gtt gat gca ggt gac gaa gtt	816
Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val	
260 265 270	
gac gca ggt agt act atg gtg agc aag ggc gag gag ctg ttc acc ggg	864
Asp Ala Gly Ser Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly	
275 280 285	
gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag	912
Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys	
290 295 300	
ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg	960
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu	
305 310 315 320	
acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc	1008
Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	
325 330 335	
acc ctc gtg acc acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac	1056
Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr	
340 345 350	
ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa	1104
Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
355 360 365	
ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac	1152
Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
370 375 380	
aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc	1200
Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
385 390 395 400	
atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg	1248
Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
405 410 415	
cac aag ctg gag tac aac tac atc agc cac aac gtc tat atc acc gcc	1296
His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala	
420 425 430	
gac aag cag aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac	1344
Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn	
435 440 445	
atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc	1392
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
450 455 460	
ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc	1440
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
465 470 475 480	

acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	1488
Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	
			485						490					495		
gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	1536
Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	
			500					505					510			
gag	ctg	tac	aag	atg	tct	act	gtc	cac	gaa	atc	ctg	tgc	aag	ctc	agc	1584
Glu	Leu	Tyr	Lys	Met	Ser	Thr	Val	His	Glu	Ile	Leu	Cys	Lys	Leu	Ser	
		515					520					525				
ttg	gag	ggt	gtt	cat	tct	aca	ccc	cca	agt	gcc	gga	tcc				1623
Leu	Glu	Gly	Val	His	Ser	Thr	Pro	Pro	Ser	Ala	Gly	Ser				
		530				535					540					

<210> 34

<211> 541

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 34

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75					80		
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala
 245 250 255
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270
 Asp Ala Gly Ser Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
 275 280 285
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 290 295 300
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 305 310 315 320
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 325 330 335
 Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr
 340 345 350
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 355 360 365
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 370 375 380
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 385 390 395 400
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 405 410 415
 His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala
 420 425 430
 Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn
 435 440 445
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 450 455 460

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 465 470 475 480

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 485 490 495

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 500 505 510

Glu Leu Tyr Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser
 515 520 525

Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 530 535 540

<210> 35
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 35
 gactacaaag acgacgacga caaa

24

<210> 36
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 36
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 37
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HA epitope

<400> 37
 tacccatacg acgtaccaga ctacgca

27

<210> 38
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HA epitope

<400> 38

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: KT3 epitope

<400> 39

ccaccagaac cagaaaca

18

<210> 40

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: KT3 epitope

<400> 40

Pro Pro Glu Pro Glu Thr

1

5

<210> 41

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Myc epitope

<400> 41

gcagaagaac aaaaattaat aagcgaagaa gactta

36

<210> 42

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Myc epitope

<400> 42

Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1

5

10

<210> 43
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <223> Description of Artificial Sequence: EYFP

<400> 43

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130				135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	

165										170										175										
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576														
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly															
180					185					190																				
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624														
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu															
195					200					205																				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672														
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe															
210					215					220																				
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	717															
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys																
225					230					235																				

<210> 44
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: EYFP

<400> 44

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35				40						45		
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75					80
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
			115				120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 45
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(717)

<220>
<223> Description of Artificial Sequence: EGFP

<400> 45
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	717
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

<210> 46
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: EGFP

<400> 46
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

<210> 47

 $\langle 220 \rangle$

<220>

<400> 47

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240
Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	717
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

<210> 48
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: EBFP

<400> 48

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 49

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (717)

<220>

<223> Description of Artificial Sequence: ECFP

<400> 49

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	acc	tgg	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180					185					190			
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
		195					200					205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	

210 215 220 717

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg' tac aag
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 50
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ECFP

<400> 50
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 51
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <223> Description of Artificial Sequence: Fred25

<400> 51
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tag	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn	
225 230 235	

<210> 52

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fred25

<400> 52

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 225 230 235

<210> 53
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase-1,4,5
 substrate recognition sequence

<400> 53
 tgggaacatg acaa

14

<210> 54
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase-1,4,5
 substrate recognition sequence

<400> 54
 Trp Glu His Asp
 1

<210> 55
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: proCaspase-1
 substrate recognition sequence

<400> 55

tggttttaaag ac

12

<210> 56

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-1
substrate recognition sequence

<400> 56

Trp Phe Lys Asp

1

<210> 57

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 57

gacgaacacg ac

12

<210> 58

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 58

Asp Glu His Asp

1

<210> 59

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 59

gacgaagttg ac

12

<210> 60
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 60
Asp Glu Val Asp
1

<210> 61
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 61
atagaaacag ac

12

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 62
Ile Glu Thr Asp
1

<210> 63
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 63
tgggtaagag ac

12

<210> 64
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 64

Trp Val Arg Asp

1

<210> 65

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 65

gtagaaatag ac

12

<210> 66

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 66

Val Glu Ile Asp

1

<210> 67

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 67

gtagaacacg ac

12

<210> 68

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

B1

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 68
Val Glu His Asp
1

<210> 69
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 69
acagaagtag ac

12

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 70
Thr Glu Val Asp
1

<210> 71
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 71
atacaagcag ac

12

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 72
Ile Gln Ala Asp
1

<210> 73
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 73
gtagaaacag ac

12

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 74
Val Glu Thr Asp
1

<210> 75
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 75
ttagaaacag ac

12

<210> 76
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 76
Leu Glu Thr Asp
1

<210> 77
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 77
ttagaacacg ac

12

<210> 78
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 78
Leu Glu His Asp
1

<210> 79
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 79
ttagaacacg ac

12

<210> 80
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 80
Leu Glu His Asp
1

<210> 81

B1

<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 81
agccaaaatt ac

12

<210> 82
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 82
Ser Gln Asn Tyr
1

<210> 83
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 83
ccaatagtac aa

12

<210> 84
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 84
Pro Ile Val Gln
1

<210> 85
<211> 12
<212> DNA
<213> Artificial Sequence

B1

<220>
<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 85
atgtttggag ga

12

<210> 86
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 86
Met Phe Gly Gly
1

<210> 87
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 87
gcaaaaaaaaa ga

12

<210> 88
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 88
Ala Lys Lys Arg
1

b1
<210> 89
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase

substrate recognition sequence

<400> 89
gtgaaaatg

9

<210> 90
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 90
Val Lys Met
1

<210> 91
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 91
gacgcagaat tc

12

<210> 92
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 92
Asp Ala Glu Phe
1

<210> 93
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 93

aaaccagcat tattc

15

<210> 94

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 94

Lys Pro Ala Leu Phe

1

5

<210> 95

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 95

ttcagatta

9

<210> 96

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 96

Phe Arg Leu

1

<210> 97

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 97

ggaccattag gacca

15

B1

<210> 98
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 98
Gly Pro Leu Gly Pro
1 5

<210> 99
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 99
atagaaccag ac

12

<210> 100
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 100
Ile Glu Pro Asp
1

<210> 101
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 101
atgcccaaga agaagccgac gcccatccag ctgaac

36

<210> 102
<211> 12
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 102

Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn
1 5 10

<210> 103

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 103

atgctggccc ggaggaagcc ggtgctgccg gcgctcacca tcaac

45

<210> 104

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 104

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn
1 5 10 15

<210> 105

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 105

gcctcgcagt ttgaaaca

18

<210> 106

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 106
Ala Ser Gln Phe Glu Thr
1 5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 107
gcttctcaat ttgaaacg

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence


<400> 108
Ala Ser Gln Phe Glu Thr
1 5

<210> 109
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 109
gccaaccaac gtgcaaca

18

 <210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 110
Ala Asn Gln Arg Ala Thr
1 5

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 111
gcttctcaat ttgaaacg

18

<210> 112
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 112
Ala Ser Gln Phe Glu Thr
1 5

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 113
acgaaaaaag ctgtgaaa

18

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 114
Thr Lys Lys Ala Val Lys
1 5

B1

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 115
gaccagaagc tctctgag

18

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 116
Asp Gln Lys Leu Ser Glu
1 5

<210> 117
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 117
atcgacagga tcatggag

18

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 118
Ile Asp Arg Ile Met Glu
1 5

<210> 119

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 119
agagaccaga agctctct

18

<210> 120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 120
Arg Asp Gln Lys Leu Ser
1 5

<210> 121
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin G substrate recognition sequence

<400> 121
acgagcgcag ccaagttg

18

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin G substrate recognition sequence

<400> 122
Thr Ser Ala Ala Lys Leu
1 5

<210> 123
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 123

atgtctactg tccacgaaat cctgtgcaag ctcagcttgg aggggtgttca ttctacaccc 60

ccaagtgcc

69

<210> 124

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 124

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val
1 5 10 15

His Ser Thr Pro Pro Ser Ala
20

<210> 125

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 125

atgggatgta cattaagcgc agaagacaaa gcagcagtag aaagaagcaa aatgatagac 60

agaaacttaa gagaagacgg agaaaaagct gctaga

96

<210> 126

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 126

Met Gly Cys Thr Leu Ser Ala Glu Asp Lys Ala Ala Val Glu Arg Ser
1 5 10 15

Lys Met Ile Asp Arg Asn Leu Arg Glu Asp Gly Glu Lys Ala Ala Arg

<210> 127
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleus target
 sequence

<400> 127
 agaaggaac gacaaaag 18

<210> 128
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleus target
 sequence

<400> 128
 Arg Arg Lys Arg Gln Lys
 1 5

<210> 129
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleolus
 target sequence

<400> 129
 agaaaacgta tacgtactta cctcaagtcc tgcaggcgga tgaaaagaag tggttttgag 60
 atgtctcgac ctattccttc ccaccttact 90

<210> 130
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleolus
 target sequence

B1

<400> 130
Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys Arg
1 5 10 15

Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr
20 25 30

<210> 131
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mitochondria
target sequence

<400> 131
atgtccgtcc tgacgccgct gctgctgcgg ggcttgacag gtcgggccg gcgggtccca 60
gtgccgcgcg ccaagatcca ttcgttg 87

<210> 132
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mitochondria
target sequence

<400> 132
Met Ser Val Leu Thr Pro Leu Leu Leu Arg Gly Leu Thr Gly Ser Ala
1 5 10 15
Arg Arg Leu Pro Val Pro Arg Ala Leu Ile His Ser Leu
20 25

<210> 133
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 133
atgagcattg ttttaataat tgttattgtg gtgatttttt taatatgttt tttatattta 60
agcaacagca aagatcccag agtaccagtt gaattaatg 99

<210> 134
<211> 33

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 134
Met Ser Ile Val Leu Ile Ile Val Ile Val Val Ile Phe Leu Ile Cys
1 5 10 15
Phe Leu Tyr Leu Ser Asn Ser Lys Asp Pro Arg Val Pro Val Glu Leu
20 25 30

Met

<210> 135
<211> 246
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Golgi target
sequence

<400> 135
atgaggcttc gggagccgct cctgagcggc agcgccgcga tgccaggcgc gtccttacag 60
cgggcctgcc gctgctcgt ggccgtctgc gctctgcacc ttggcgtcac cctcgtttac 120
tacctggctg gccgcgacct gagccgctg ccccaactgg tcggagtctc cacaccgctg 180
cagggcggct cgaacagtgc cgccgccatc gggcagtcct ccggggagct ccggaccgga 240
ggggcc 246

<210> 136
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Golgi target
sequence

<400> 136
Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
1 5 10 15
Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
20 25 30
His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
35 40 45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
 50 55 60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
 65 70 75 80

Gly Ala

<210> 137
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Endoplasmic
 reticulum target sequence

<400> 137
 gaaacaataa gacctataag aataagaaga tgttcttatt ttacatctac agacagcaaa 60
 atggcaattc aattaagatc tccctttcca ttagcattac caggaatgtt agctttatta 120
 ggatgggtggg ggtttttcag tagaaaaaaa 150

<210> 138
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Endoplasmic
 reticulum target sequence

<400> 138
 Glu Thr Ile Arg Pro Ile Arg Ile Arg Arg Cys Ser Tyr Phe Thr Ser
 1 5 10 15
 Thr Asp Ser Lys Met Ala Ile Gln Leu Arg Ser Pro Phe Pro Leu Ala
 20 25 30
 Leu Pro Gly Met Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg
 35 40 45
 Lys Lys
 50

b1
 <210> 139
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 139

gccttgacaga agaagctgga ggagctagag ctgatgag

39

<210> 140

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 140

Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

<210> 141

<211> 1024

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Size exclusion
target sequence

<400> 141

gccgacctca gtcttggtga tgcgttgaca gaaccacctc cagaaattga gggagaaata 60
aagcgagact tcatggctgc gctggaggca gagccctatg atgacatcgt gggagaaact 120
gtggagaaaa ctgagtttat tcctctcctg gatggtgatg agaaaaccgg gaactcagag 180
tccaaaaaga aaccctgctt agacactagc caggttgaag gtatcccatc ttctaaacca 240
acactcctag ccaatggtga tcatggaatg gaggggaata acactgcagg gtctccaact 300
gacttccttg aagagagagt ggactatccg gattatcaga gcagccagaa ctggccagaa 360
gatgcaagct tttgtttcca gcctcagcaa gtgtagata ctgaccaggc tgagcccttt 420
aacgagcacc gtgatgatgg tttggcagat ctgctctttg tctccagtgg acccacgaac 480
gcttctgcat ttacagagcg agacaatcct tcagaagaca gttacggtat gcttccctgt 540
gactcatttg cttccacggc tggtgtatct caggagtggc ctgtgggagc cccaaactct 600
ccatgttcag agtcctgtgt ctccccagag gttactatag aaaccctaca gccagcaaca 660
gagctctcca aggcagcaga agtggaatca gtgaaagagc agctgccagc taaagcattg 720
gaaacgatgg cagagcagac cactgatgtg gtgcactctc catccacaga cacaacacca 780

ggcccagaca cagaggcagc actggctaaa gacatagaag agatcaccaa gccagatgtg 840
atattggcaa atgtcacgca gccatctact gaatcgata tggtcctggc ccaggacatg 900
gaactactca caggaacaga ggcagccac gctaacaata tcatattgcc tacagaacca 960
gacgaatctt caaccaagga tgtagcacca cctatggaag aagaaattgt cccaggcaat 1020
gata 1024

<210> 142
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Size exclusion
target sequence

<400> 142
Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile
1 5 10 15
Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro
20 25 30
Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro
35 40 45
Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys
50 55 60
Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro
65 70 75 80
Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala
85 90 95
Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr
100 105 110
Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro
115 120 125
Gln Gln Val Leu Asp Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg
130 135 140
Asp Asp Gly Leu Ala Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn
145 150 155 160
Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly
165 170 175
Met Leu Pro Cys Asp Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu
180 185 190

B1

Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser
 195 200 205
 Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys
 210 215 220
 Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu
 225 230 235 240
 Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser Thr
 245 250 255
 Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile
 260 265 270
 Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro
 275 280 285
 Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr
 290 295 300
 Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro
 305 310 315 320
 Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile
 325 330 335
 Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu
 340 345 350
 Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys
 355 360 365
 Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile
 370 375 380
 Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val
 385 390 395 400
 Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu
 405 410 415
 Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr
 420 425 430
 Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser
 435 440 445
 Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu
 450 455 460
 Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu
 465 470 475 480
 Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala
 485 490 495

Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val
 500 505 510
 Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn
 515 520 525
 Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala
 530 535 540
 Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val
 545 550 555 560
 Pro Ile Lys Asp Lys Gly
 565

<210> 143
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Vesicle
 membrane target sequence

<400> 143
 atgtgggcaa tcgggattac tggtctgggtt atcttcatca tcatcatcat cgtgtggggtt 60
 gtc 63

<210> 144
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Vesicle
 membrane target sequence

<400> 144
 Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe Ile Ile Ile Ile
 1 5 10 15
 Ile Val Trp Val Val
 20

<210> 145
 <211> 61
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Vesicle
 membrane target sequence

B1

<400> 145
atgtgggcga tagggatcag tgccttggtg atcattgtca tcatcatcat cgtgtggtgt 60

g 61

<210> 146
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 146
Met Trp Ala Ile Gly Ile Ser Val Leu Val Ile Ile Val Ile Ile Ile
1 5 10 15

Ile Val Trp Cys
20

<210> 147
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 147
gacctgcaga agaagctgga ggagctggaa cttgacgag 39

<210> 148
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 148
Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

b1
<210> 149
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peroxisome

target sequence

<400> 149

tctaaactg

9

<210> 150

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peroxisome
target sequence

<400> 150

Ser Lys Leu

1

<210> 151

<211> 3378

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(3375)

<400> 151

atg gcc gac ctc agt ctt gtg gat gcg ttg aca gaa cca cct cca gaa	48
Met Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu	
1 5 10 15	

att gag gga gaa ata aag cga gac ttc atg gct gcg ctg gag gca gag	96
Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu	
20 25 30	

ccc tat gat gac atc gtg gga gaa act gtg gag aaa act gag ttt att	144
Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile	
35 40 45	

cct ctc ctg gat ggt gat gag aaa acc ggg aac tca gag tcc aaa aag	192
Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys	
50 55 60	

aaa ccc tgc tta gac act agc cag gtt gaa ggt atc cca tct tct aaa	240
Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys	
65 70 75 80	

B1

cca aca ctc cta gcc aat ggt gat cat gga atg gag ggg aat aac act	288
Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr	
85 90 95	

gca ggg tct cca act gac ttc ctt gaa gag aga gtg gac tat ccg gat	336
Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp	
100 105 110	

tat	cag	agc	agc	cag	aac	tgg	cca	gaa	gat	gca	agc	ttt	tgt	ttc	cag	384
Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp	Ala	Ser	Phe	Cys	Phe	Gln	
		115					120					125				
cct	cag	caa	gtg	tta	gat	act	gac	cag	gct	gag	ccc	ttt	aac	gag	cac	432
Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala	Glu	Pro	Phe	Asn	Glu	His	
		130				135					140					
cgt	gat	gat	ggg	ttg	gca	gat	ctg	ctc	ttt	gtc	tcc	agt	gga	ccc	acg	480
Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe	Val	Ser	Ser	Gly	Pro	Thr	
145					150					155					160	
aac	gct	tct	gca	ttt	aca	gag	cga	gac	aat	cct	tca	gaa	gac	agt	tac	528
Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn	Pro	Ser	Glu	Asp	Ser	Tyr	
				165					170					175		
ggg	atg	ctt	ccc	tgt	gac	tca	ttt	gct	tcc	acg	gct	gtt	gta	tct	cag	576
Gly	Met	Leu	Pro	Cys	Asp	Ser	Phe	Ala	Ser	Thr	Ala	Val	Val	Ser	Gln	
			180					185					190			
gag	tgg	tct	gtg	gga	gcc	cca	aac	tct	cca	tgt	tca	gag	tcc	tgt	gtc	624
Glu	Trp	Ser	Val	Gly	Ala	Pro	Asn	Ser	Pro	Cys	Ser	Glu	Ser	Cys	Val	
		195					200					205				
tcc	cca	gag	gtt	act	ata	gaa	acc	cta	cag	cca	gca	aca	gag	ctc	tcc	672
Ser	Pro	Glu	Val	Thr	Ile	Glu	Thr	Leu	Gln	Pro	Ala	Thr	Glu	Leu	Ser	
		210				215					220					
aag	gca	gca	gaa	gtg	gaa	tca	gtg	aaa	gag	cag	ctg	cca	gct	aaa	gca	720
Lys	Ala	Ala	Glu	Val	Glu	Ser	Val	Lys	Glu	Gln	Leu	Pro	Ala	Lys	Ala	
225					230				235					240		
ttg	gaa	acg	atg	gca	gag	cag	acc	act	gat	gtg	gtg	cac	tct	cca	tcc	768
Leu	Glu	Thr	Met	Ala	Glu	Gln	Thr	Thr	Asp	Val	Val	His	Ser	Pro	Ser	
				245					250					255		
aca	gac	aca	aca	cca	ggc	cca	gac	aca	gag	gca	gca	ctg	gct	aaa	gac	816
Thr	Asp	Thr	Thr	Pro	Gly	Pro	Asp	Thr	Glu	Ala	Ala	Leu	Ala	Lys	Asp	
				260				265					270			
ata	gaa	gag	atc	acc	aag	cca	gat	gtg	ata	ttg	gca	aat	gtc	acg	cag	864
Ile	Glu	Glu	Ile	Thr	Lys	Pro	Asp	Val	Ile	Leu	Ala	Asn	Val	Thr	Gln	
		275					280					285				
cca	tct	act	gaa	tcg	gat	atg	ttc	ctg	gcc	cag	gac	atg	gaa	cta	ctc	912
Pro	Ser	Thr	Glu	Ser	Asp	Met	Phe	Leu	Ala	Gln	Asp	Met	Glu	Leu	Leu	
		290				295					300					
aca	gga	aca	gag	gca	gcc	cac	gct	aac	aat	atc	ata	ttg	cct	aca	gaa	960
Thr	Gly	Thr	Glu	Ala	Ala	His	Ala	Asn	Asn	Ile	Ile	Leu	Pro	Thr	Glu	
305					310					315					320	
cca	gac	gaa	tct	tca	acc	aag	gat	gta	gca	cca	cct	atg	gaa	gaa	gaa	1008
Pro	Asp	Glu	Ser	Ser	Thr	Lys	Asp	Val	Ala	Pro	Pro	Met	Glu	Glu	Glu	
				325					330					335		

att gtc cca ggc aat gat acg aca tcc ccc aaa gaa aca gag aca aca	1056
Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr	
340 345 350	
ctt cca ata aaa atg gac ttg gca cca cct gag gat gtg tta ctt acc	1104
Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr	
355 360 365	
aaa gaa aca gaa cta gcc cca gcc aag ggc atg gtt tca ctc tca gaa	1152
Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu	
370 375 380	
ata gaa gag gct ctg gca aag aat gat gtt cgc tct gca gaa ata cct	1200
Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro	
385 390 395 400	
gtg gct cag gag aca gtg gtc tca gaa aca gag gtg gtc ctg gca aca	1248
Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr	
405 410 415	
gaa gtg gta ctg ccc tca gat ccc ata aca aca ttg aca aag gat gtg	1296
Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val	
420 425 430	
aca ctc ccc tta gaa gca gag aga ccg ttg gtg acg gac atg act cca	1344
Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro	
435 440 445	
tct ctg gaa aca gaa atg acc cta ggc aaa gag aca gct cca ccc aca	1392
Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr	
450 455 460	
gaa aca aat ttg ggc atg gcc aaa gac atg tct cca ctc cca gaa tca	1440
Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser	
465 470 475 480	
gaa gtg act ctg ggc aag gac gtg gtt ata ctt cca gaa aca aag gtg	1488
Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val	
485 490 495	
gct gag ttt aac aat gtg act cca ctt tca gaa gaa gag gta acc tca	1536
Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser	
500 505 510	
gtc aag gac atg tct ccg tct gca gaa aca gag gct ccc ctg gct aag	1584
Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys	
515 520 525	
aat gct gat ctg cac tca gga aca gag ctg att gtg gac aac agc atg	1632
Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met	
530 535 540	
gct cca gcc tcc gat ctt gca ctg ccc ttg gaa aca aaa gta gca aca	1680
Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr	
545 550 555 560	
gtt cca att aaa gac aaa gga act gta cag act gaa gaa aaa cca cgt	1728

B1

Val	Pro	Ile	Lys	Asp	Lys	Gly	Thr	Val	Gln	Thr	Glu	Glu	Lys	Pro	Arg		
				565					570					575			
gaa	gac	tcc	cag	tta	gca	tct	atg	cag	cac	aag	gga	cag	tca	aca	gta	1776	
Glu	Asp	Ser	Gln	Leu	Ala	Ser	Met	Gln	His	Lys	Gly	Gln	Ser	Thr	Val		
			580					585				590					
cct	cct	tgc	acg	gct	tca	cca	gaa	cca	gtc	aaa	gct	gca	gaa	caa	atg	1824	
Pro	Pro	Cys	Thr	Ala	Ser	Pro	Glu	Pro	Val	Lys	Ala	Ala	Glu	Gln	Met		
		595					600					605					
tct	acc	tta	cca	ata	gat	gca	cct	tct	cca	tta	gag	aac	tta	gag	cag	1872	
Ser	Thr	Leu	Pro	Ile	Asp	Ala	Pro	Ser	Pro	Leu	Glu	Asn	Leu	Glu	Gln		
	610					615					620						
aag	gaa	acg	cct	ggc	agc	cag	cct	tct	gag	cct	tgc	tca	gga	gta	tcc	1920	
Lys	Glu	Thr	Pro	Gly	Ser	Gln	Pro	Ser	Glu	Pro	Cys	Ser	Gly	Val	Ser		
625					630				635						640		
cgg	caa	gaa	gaa	gca	aag	gct	gct	gta	ggg	gtg	act	gga	aat	gac	atc	1968	
Arg	Gln	Glu	Glu	Ala	Lys	Ala	Ala	Val	Gly	Val	Thr	Gly	Asn	Asp	Ile		
				645					650					655			
act	acc	ccg	cca	aac	aag	gag	cca	cca	cca	agc	cca	gaa	aag	aaa	gca	2016	
Thr	Thr	Pro	Pro	Asn	Lys	Glu	Pro	Pro	Pro	Ser	Pro	Glu	Lys	Lys	Ala		
			660					665					670				
aag	cct	ttg	gcc	acc	act	caa	cct	gca	aag	act	tca	aca	tcg	aaa	gcc	2064	
Lys	Pro	Leu	Ala	Thr	Thr	Gln	Pro	Ala	Lys	Thr	Ser	Thr	Ser	Lys	Ala		
		675					680					685					
aaa	aca	cag	ccc	act	tct	ctc	cct	aag	caa	cca	gct	ccc	acc	acc	tct	2112	
Lys	Thr	Gln	Pro	Thr	Ser	Leu	Pro	Lys	Gln	Pro	Ala	Pro	Thr	Thr	Ser		
	690					695					700						
ggg	ggg	ttg	aat	aaa	aaa	ccc	atg	agc	ctc	gcc	tca	ggc	tca	gtg	cca	2160	
Gly	Gly	Leu	Asn	Lys	Lys	Pro	Met	Ser	Leu	Ala	Ser	Gly	Ser	Val	Pro		
705					710					715					720		
gct	gcc	cca	cac	aaa	cgc	cct	gct	gct	gcc	act	gct	act	gcc	agg	cct	2208	
Ala	Ala	Pro	His	Lys	Arg	Pro	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Arg	Pro		
				725					730					735			
tcc	acc	cta	cct	gcc	aga	gac	gtg	aag	cca	aag	cca	att	aca	gaa	gct	2256	
Ser	Thr	Leu	Pro	Ala	Arg	Asp	Val	Lys	Pro	Lys	Pro	Ile	Thr	Glu	Ala		
			740					745					750				
aag	gtt	gcc	gaa	aag	cgg	acc	tct	cca	tcc	aag	cct	tca	tct	gcc	cca	2304	
Lys	Val	Ala	Glu	Lys	Arg	Thr	Ser	Pro	Ser	Lys	Pro	Ser	Ser	Ala	Pro		
		755					760					765					
gcc	ctc	aaa	cct	gga	cct	aaa	acc	acc	cca	acc	gtt	tca	aaa	gcc	aca	2352	
Ala	Leu	Lys	Pro	Gly	Pro	Lys	Thr	Thr	Pro	Thr	Val	Ser	Lys	Ala	Thr		
		770				775					780						
tct	ccc	tca	act	ctt	gtt	tcc	act	gga	cca	agt	agt	aga	agt	cca	gct	2400	
Ser	Pro	Ser	Thr	Leu	Val	Ser	Thr	Gly	Pro	Ser	Ser	Arg	Ser	Pro	Ala		

B1

785		790		795		800	
aca act ctg cct aag agg cca acc agc atc aag act gag ggg aaa cct	2448						
Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro							
		805		810		815	
gct gat gtc aaa agg atg act gct aag tct gcc tca gct gac ttg agt	2496						
Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser							
		820		825		830	
cgc tca aag acc acc tct gcc agt tct gtg aag aga aac acc act ccc	2544						
Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro							
		835		840		845	
act ggg gca gca ccc cca gca ggg atg act tcc act cga gtc aag ccc	2592						
Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro							
		850		855		860	
atg tct gca cct agc cgc tct tct ggg gct ctt tct gtg gac aag aag	2640						
Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys							
		865		870		875	880
ccc act tcc act aag cct agc tcc tct gct ccc agg gtg agc cgc ctg	2688						
Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala Pro Arg Val Ser Arg Leu							
		885		890		895	
gcc aca act gtt tct gcc cct gac ctg aag agt gtt cgc tcc aag gtc	2736						
Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val							
		900		905		910	
ggc tct aca gaa aac atc aaa cac cag cct gga gga ggc cgg gcc aaa	2784						
Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Gly Arg Ala Lys							
		915		920		925	
gta gag aaa aaa aca gag gca gct acc aca gct ggg aag cct gaa cct	2832						
Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro							
		930		935		940	
aat gca gtc act aaa gca gcc ggc tcc att gcg agt gca cag aaa ccg	2880						
Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro							
		945		950		955	960
cct gct ggg aaa gtc cag ata gta tcc aaa aaa gtg agc tac agt cat	2928						
Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His							
		965		970		975	
att caa tcc aag tgt gtt tcc aag gac aat att aag cat gtc cct gga	2976						
Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly							
		980		985		990	
tgt ggc aat gtt cag att cag aac aag aaa gtg gac ata tcc aag gtc	3024						
Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val							
		995		1000		1005	
tcc tcc aag tgt ggg tcc aaa gct aat atc aag cac aag cct ggt gga	3072						
Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly							
		1010		1015		1020	

gga gat gtc aag att gaa agt cag aag ttg aac ttc aag gag aag gcc 3120
 Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala
 1025 1030 1035 1040

caa gcc aaa gtg gga tcc ctt gat aac gtt ggc cac ttt cct gca gga 3168
 Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly
 1045 1050 1055

ggt gcc gtg aag act gag ggc ggt ggc agt gag gcc ctt ccg tgt cca 3216
 Gly Ala Val Lys Thr Glu Gly Gly Gly Ser Glu Ala Leu Pro Cys Pro
 1060 1065 1070

ggc ccc ccc gct ggg gag gag cca gtc atc cct gag gct gcg cct gac 3264
 Gly Pro Pro Ala Gly Glu Glu Pro Val Ile Pro Glu Ala Ala Pro Asp
 1075 1080 1085

cgt ggc gcc cct act tca gcc agt ggc ctc agt ggc cac acc acc ctg 3312
 Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu
 1090 1095 1100

tca ggg ggt ggt gac caa agg gag ccc cag acc ttg gac agc cag atc 3360
 Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln Thr Leu Asp Ser Gln Ile
 1105 1110 1115 1120

cag gag aca agc atc taa 3378
 Gln Glu Thr Ser Ile
 1125

<210> 152
 <211> 1125
 <212> PRT
 <213> Mus musculus

<400> 152
 Met Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu
 1 5 10 15

Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu
 20 25 30

Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile
 35 40 45

Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys
 50 55 60

Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys
 65 70 75 80

Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr
 85 90 95

Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp
 100 105 110

B1

Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln
 115 120 125
 Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu Pro Phe Asn Glu His
 130 135 140
 Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val Ser Ser Gly Pro Thr
 145 150 155 160
 Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr
 165 170 175
 Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr Ala Val Val Ser Gln
 180 185 190
 Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val
 195 200 205
 Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser
 210 215 220
 Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala
 225 230 235 240
 Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser
 245 250 255
 Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp
 260 265 270
 Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln
 275 280 285
 Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu
 290 295 300
 Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu
 305 310 315 320
 Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu
 325 330 335
 Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr
 340 345 350
 Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr
 355 360 365
 Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu
 370 375 380
 Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro
 385 390 395 400
 Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr
 405 410 415

Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val
 420 425 430
 Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro
 435 440 445
 Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr
 450 455 460
 Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser
 465 470 475 480
 Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val
 485 490 495
 Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser
 500 505 510
 Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys
 515 520 525
 Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met
 530 535 540
 Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr
 545 550 555 560
 Val Pro Ile Lys Asp Lys Gly Thr Val Gln Thr Glu Glu Lys Pro Arg
 565 570 575
 Glu Asp Ser Gln Leu Ala Ser Met Gln His Lys Gly Gln Ser Thr Val
 580 585 590
 Pro Pro Cys Thr Ala Ser Pro Glu Pro Val Lys Ala Ala Glu Gln Met
 595 600 605
 Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro Leu Glu Asn Leu Glu Gln
 610 615 620
 Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu Pro Cys Ser Gly Val Ser
 625 630 635 640
 Arg Gln Glu Glu Ala Lys Ala Ala Val Gly Val Thr Gly Asn Asp Ile
 645 650 655
 Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro Ser Pro Glu Lys Lys Ala
 660 665 670
 Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys Thr Ser Thr Ser Lys Ala
 675 680 685
 Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln Pro Ala Pro Thr Thr Ser
 690 695 700
 Gly Gly Leu Asn Lys Lys Pro Met Ser Leu Ala Ser Gly Ser Val Pro
 705 710 715 720

Ala Ala Pro His Lys Arg Pro Ala Ala Ala Thr Ala Thr Ala Arg Pro
 725 730 735
 Ser Thr Leu Pro Ala Arg Asp Val Lys Pro Lys Pro Ile Thr Glu Ala
 740 745 750
 Lys Val Ala Glu Lys Arg Thr Ser Pro Ser Lys Pro Ser Ser Ala Pro
 755 760 765
 Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro Thr Val Ser Lys Ala Thr
 770 775 780
 Ser Pro Ser Thr Leu Val Ser Thr Gly Pro Ser Ser Arg Ser Pro Ala
 785 790 795 800
 Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro
 805 810 815
 Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser
 820 825 830
 Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro
 835 840 845
 Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro
 850 855 860
 Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys
 865 870 875 880
 Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala Pro Arg Val Ser Arg Leu
 885 890 895
 Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val
 900 905 910
 Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Gly Arg Ala Lys
 915 920 925
 Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro
 930 935 940
 Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro
 945 950 955 960
 Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His
 965 970 975
 Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly
 980 985 990
 Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val
 995 1000 1005
 Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly
 1010 1015 1020

Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala
 1025 1030 1035 1040
 Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly
 1045 1050 1055
 Gly Ala Val Lys Thr Glu Gly Gly Gly Ser Glu Ala Leu Pro Cys Pro
 1060 1065 1070
 Gly Pro Pro Ala Gly Glu Glu Pro Val Ile Pro Glu Ala Ala Pro Asp
 1075 1080 1085
 Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu
 1090 1095 1100
 Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln Thr Leu Asp Ser Gln Ile
 1105 1110 1115 1120
 Gln Glu Thr Ser Ile
 1125

<210> 153
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 153
 tcatcatccg gagctggagc cggagctggc cgatcggctg ttaaactctga aggaaagaga 60
 aagtgtgacg aagttgatgg aattgatgaa gtagca 96

<210> 154
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 154
 gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
 gatttcgtgg acagtagaca tagtacttgc tacttcatc 99

<210> 155
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 155

tcatcatccg gagctgga

18

<210> 156

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 156

gaagaaggat ccggcact

18

<210> 157

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 157

tcatcatccg gaagaaggaa acgacaaaag cgatcggctg ttaaactctga aggaaagaga 60

aagtgtgacg aagttgatgg aattgatgaa gtagca

96

<210> 158

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 158

tcatcatccg gaagaagg

18

<210> 159

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 159
tcatcatccg gaagaaggaa acgacaaaag cgatcgacaa gacttggtga aattgacaac 60

<210> 160
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 160
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactggt gtcaatttc 99

<210> 161
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 161
tcatcatccg gaagaaggaa acgacaaaag cgatcgatc aaaaaggaat accagttgaa 60
acagacagcg aagagcaacc ttat 84

<210> 162
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 162
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactata aggttgctc 99

<210> 163
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

oligonucleotide

<400> 163

tcatcatccg gaagaaaacg tatacgtact tacctcaagt cctgcaggcg gatgaaaaga 60

<210> 164

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 164

gaagaacgat cgagtaaggt gggaaggaat aggtcgagac atctcaaaac cacttctttt 60

cat

63

<210> 165

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 165

tcatcatccg gaagaaaa

18

<210> 166

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 166

gaagaacgat cgagtaag

18

<210> 167

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 167

ttagaacatg acaa

14

<210> 168

<211> 4

<212> PRT

<213> Artificial Sequence

*BI
Concld* <220>

<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 168

Leu Glu His Asp

1